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(54) Title: NOVEL HUMAN β_2 INTEGRIN ALPHA SUBUNIT

(57) Abstract

DNA encoding a novel human β_2 integrin α subunit polypeptide, designated α_d, is disclosed along with methods and materials for production of the same by recombinant procedures. Fusion proteins are also disclosed which include extracellular α_d protein fragments, α_d I domain fragments or full length α_d polypeptides and human immunoglobulin constant regions. Binding molecules specific for α_d are also disclosed as useful for modulating the biological activities of α_d. DNA from other species which show homology to human α_d encoding sequences are also disclosed.

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Novel Human β_2 Integrin Alpha Subunit

This application is a continuation-in-part of U.S. Application Serial No. 08/286,889, filed August 5, 1994, which is pending, which in turn is a continuation-in-part of U.S. Application Serial No. 08/173,497, filed December 23, 1993, which is pending.

Field of the Invention

The present invention relates to the cloning and expression of polynucleotides encoding a novel human β_2 integrin α subunit, designated α_d, which is structurally related to the known human β_2 integrin α subunits, CD11a, CD11b and CD11c. The present invention also relates to polynucleotides isolated from other species which show homology to human α_d encoding sequences.

Background of the Invention

The integrins are a class of membrane-associated molecules which actively participate in cellular adhesion. Integrins are transmembrane heterodimers comprising an α subunit in noncovalent association with a β subunit. To date, at least fourteen α subunits and eight β subunits have been identified [reviewed in Springer, *Nature 346*:425-434 (1990)]. The β subunits are generally capable of association with more than one α subunit and the heterodimers sharing a common β subunit have been classified as subfamilies within the integrin population.

One class of human integrins, restricted to expression in white blood cells, is characterized by a common β_2 subunit. As a result of this cell-specific expression, these integrins are commonly referred to as the leukocyte integrins, Leu-CAMs or leukointegrins. Because of the common β_2 subunit, an alternative designation of this class is the β_2 integrins. The β_2 subunit (CD18) has previously been isolated in association with one of three distinct α subunits,

CD11a, CD11b or CD11c. The isolation of a cDNA encoding human CD18 is described in Kishimoto, *et al., Cell 48*:681-690 (1987). In official WHO nomenclature, the heterodimeric proteins are referred to as CD11a/CD18, CD11b/CD18, and CD11c/CD18; in common nomenclature they are referred to as LFA-1, Mac-1 or Mo1 and p150,95 or LeuM5, respectively [Cobbold, *et al.*, in *Leukocyte Typing III*, McMichael (ed), Oxford Press, p.788 (1987)]. The human β_2 integrin α subunits CD11a, CD11b and CD11c have been demonstrated to migrate under reducing condition in electrophoresis with apparent molecular weights of approximately 180 kD, 155 kD and 150 kD, respectively, and DNAs encoding these subunits have been cloned [CD11a, Larson, *et al., J.Cell Biol. 108*:703-712 (1989); CD11b, Corbi, *et al., J.Biol.Chem. 263*:12403-12411 (1988) and CD11c, Corbi, *et al. EMBO J. 6*:4023-4028 (1987)]. Putative homologs of the human β_2 integrin α and β chains, defined by approximate similarity in molecular weight, have been variously identified in other species including monkeys and other primates [Letvin, *et al., Blood 61*:408-410 (1983)], mice [Sanchez-Madrid, *et al., J.Exp.Med. 154*:1517 (1981)], and dogs [Moore, *et al., Tissue Antigens 36*:211-220 (1990)].

The absolute molecular weights of presumed homologs from other species have been shown to vary significantly [see, *e.g.*, Danilenko *et al., Tissue Antigens 40*:13-21 (1992)], and in the absence of sequence information, a definitive correlation between human integrin subunits and those identified in other species has not been possible. Moreover, variation in the number of members in a protein family has been observed between different species. Consider, for example, that more IgA isotypes have been isolated in rabbits than in humans [Burnett, *et al., EMBO J. 8*:4041-4047 (1989) and Schneiderman, *et al., Proc.Natl.Acad.Sci.(USA) 86*:7561-7565 (1989)]. Similarly, in humans, at least six variants of the metallothionine protein have been previously identified [Karin and Richards, *Nature 299*:797-802 (1982) and Varshney, *et al., Mol.Cell.Biol. 6*:26-37, (1986)], whereas in the mouse, only two such variants are

in evidence [Searle, *et al.*, *Mol.Cell.Biol.* *4*:1221-1230 (1984)]. Therefore, existence of multiple members of a protein family in one species does not necessarily imply that corresponding family members exist in another species.

In the specific context of β_2 integrins, in dogs it has been observed that the presumed canine β_2 counterpart to the human CD18 is capable of dimer formation with as many as four potentially distinct α subunits [Danilenko, *et al.*, *supra*]. Antibodies generated by immunizing mice with canine splenocytes resulted in monoclonal antibodies which immunoprecipitated proteins tentatively designated as canine homologs to human CD18, CD11a, CD11b and CD11c based mainly on similar, but not identical, molecular weights. Another anti-canine splenocyte antibody, Ca11.8H2, recognized and immunoprecipitated a fourth α-like canine subunit also capable of association with the β_2 subunit, but having a unique molecular weight and restricted in expression to a subset of differentiated tissue macrophages. Antibodies generated by immunization of hamsters with murine dendritic cells resulted in two anti-integrin antibodies [Metlay, *et al.*, *J.Exp.Med.* *171*:1753-1771 (1990)]. One antibody, 2E6, immunoprecipitated a predominant heterodimer with subunits having approximate molecular weights of 180 kD and 90 kD in addition to minor bands in the molecular weight range of 150-160 kD. The second antibody, N418, precipitated another apparent heterodimer with subunits having approximate molecular weights of 150 kD and 90 Kd. Based on cellular adhesion blocking studies, it was hypothesized that antibody 2E6 recognized a murine counterpart to human CD18. While the molecular weight of the N418 antigen suggested recognition of a murine homolog to human CD11c/CD18, further analysis indicated that the murine antigen exhibited a tissue distribution pattern which was inconsistent with that observed for human CD11c/CD18.

The antigens recognized by the canine Ca11.8H2 antibody and the murine N418 antibody could represent a variant species (*e.g.*, a glycosylation or splice variant) of a previously identified canine or murine α subunit.

Alternatively, these antigens may represent unique canine and murine integrin α subunits. In the absence of specific information regarding primary structure, these alternatives cannot be distinguished.

In humans, CD11a/CD18 is expressed on all leukocytes. CD11b/CD18 and CD11c/CD18 are essentially restricted to expression on monocytes, granulocytes, macrophages and natural killer (NK) cells, but CD11c/CD18 is also detected on some B-cell types. In general, CD11a/CD18 predominates on lymphocytes, CD11b/CD18 on granulocytes and CD11c/CD18 on macrophages [see review, Arnaout, *Blood 75*:1037-1050 (1990)]. Expression of the α chains, however, is variable with regard to the state of activation and differentiation of the individual cell types [See review, Larson and Springer, *Immunol.Rev.* 114:181-217 (1990).]

The involvement of the β_2 integrins in human immune and inflammatory responses has been demonstrated using monoclonal antibodies which are capable of blocking β_2 integrin-associated cell adhesion. For example, CD11a/CD18, CD11b/CD18 and CD11c/CD18 actively participate in natural killer (NK) cell binding to lymphoma and adenocarcinoma cells [Patarroyo, *et al.*, *Immunol.Rev.* 114:67-108 (1990)], granulocyte accumulation [Nourshargh, *et al.*, *J.Immunol. 142*:3193-3198 (1989)], granulocyte-independent plasma leakage [Arfors, *et al.*, *Blood 69*:338-340 (1987)], chemotactic response of stimulated leukocytes [Arfors, *et al.*, *supra*] and leukocyte adhesion to vascular endothelium [Price, *et al.*, *J.Immunol. 139*:4174-4177 (1987) and Smith, *et al.*, *J.Clin.Invest. 83*:2008-2017 (1989)]. The fundamental role of β_2 integrins in immune and inflammatory responses is made apparent in the clinical syndrome referred to as leukocyte adhesion deficiency (LAD), wherein clinical manifestations include recurrent and often life threatening bacterial infections. LAD results from heterogeneous mutations in the β_2 subunit [Kishimoto, *et al.*, *Cell 50*:193-202 (1987)] and the severity of the disease state is proportional to the degree of the

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deficiency in β_2 subunit expression. Formation of the complete integrin heterodimer is impaired by the β_2 mutation [Kishimoto, *et al., supra*].

Interestingly, at least one antibody specific for CD18 has been shown to inhibit human immunodeficiency virus type-1 (HIV-1) syncytia formation *in vitro*, albeit the exact mechanism of this inhibition is unclear [Hildreth and Orentas, *Science 244*:1075-1078 (1989)]. This observation is consistent with the discovery that a principal counterreceptor of CD11a/CD18, ICAM-1, is also a surface receptor for the major group of rhinovirus serotypes [Greve, *et al., Cell 56*:839 (1989)].

The significance of β_2 integrin binding activity in human immune and inflammatory responses underscores the necessity to develop a more complete understanding of this class of surface proteins. Identification of yet unknown members of this subfamily, as well as their counterreceptors, and the generation of monoclonal antibodies or other soluble factors which can alter biological activity of the β_2 integrins will provide practical means for therapeutic intervention in β_2 integrin-related immune and inflammatory responses.

Brief Description of the Invention

In one aspect, the present invention provides novel purified and isolated polynucleotides (*e.g.*, DNA and RNA transcripts, both sense and anti-sense strands) encoding a novel human β_2 integrin α subunit, α_d, and variants thereof (*i.e.*, deletion, addition or substitution analogs) which possess binding and/or immunological properties inherent to α_d. Preferred DNA molecules of the invention include cDNA, genomic DNA and wholly or partially chemically synthesized DNA molecules. A presently preferred polynucleotide is the DNA as set forth in SEQ ID NO: 1, encoding the polypeptide of SEQ ID NO: 2. Also provided are recombinant plasmid and viral DNA constructions (expression constructs) which include α_d encoding sequences, wherein the α_d encoding

sequence is operatively linked to a homologous or heterologous transcriptional regulatory element or elements.

Also provided by the present invention are isolated and purified mouse and rat polynucleotides which exhibit homology to polynucleotides encoding human α_d. A preferred mouse polynucleotide is set forth in SEQ ID NO: 52; a preferred rat polynucleotide is set forth in SEQ ID NO: 54.

As another aspect of the invention, prokaryotic or eukaryotic host cells transformed or transfected with DNA sequences of the invention are provided which express α_d polypeptide or variants thereof. Host cells of the invention are particularly useful for large scale production of α_d polypeptide, which can be isolated from either the host cell itself or from the medium in which the host cell is grown. Host cells which express α_d polypeptide on their extracellular membrane surface are also useful as immunogens in the production of α_d-specific antibodies. Preferably, host cells transfected with α_d will be co-transfected to express a β_2 integrin subunit in order to allow surface expression of the heterodimer.

Also provided by the present invention are purified and isolated α_d polypeptides, fragments and variants thereof. Preferred α_d polypeptides are as set forth in SEQ ID NO: 2. Novel α_d products of the invention may be obtained as isolates from natural sources, but, along with α_d variant products, are preferably produced by recombinant procedures involving host cells of the invention. Completely glycosylated, partially glycosylated and wholly de-glycosylated forms of the α_d polypeptide may be generated by varying the host cell selected for recombinant production and/or post-isolation processing. Variant α_d polypeptides of the invention may comprise water soluble and insoluble α_d polypeptides including analogs wherein one or more of the amino acids are deleted or replaced: (1) without loss, and preferably with enhancement, of one or more biological activities or immunological characteristics specific for α_d; or (2) with specific disablement of a particular ligand/receptor binding or signalling

library. Alternatively, polymerase chain reaction (PCR) using oligonucleotide primers that are designed based on the known cDNA sequence can be used to amplify and identify genomic α_d DNA sequences. Synthetic DNAs encoding the α_d polypeptide, including fragments and other variants thereof, may be produced by conventional synthesis methods.

DNA sequence information of the invention also makes possible the development, by homologous recombination or "knockout" strategies [see, *e.g.*, Kapecchi, *Science 244*:1288-1292 (1989)], to produce rodents that fail to express a functional α_d polypeptide or that express a variant α_d polypeptide. Such rodents are useful as models for studying the activities of α_d and α_d modulators *in vivo*.

DNA and amino acid sequences of the invention also make possible the analysis of α_d epitopes which actively participate in counterreceptor binding as well as epitopes which may regulate, rather than actively participate in, binding. Identification of epitopes which may participate in transmembrane signal transduction is also comprehended by the invention.

DNA of the invention is also useful for the detection of cell types which express α_d polypeptide. Standard DNA/RNA hybridization techniques which utilize α_d DNA to detect α_d RNA may be used to determine the constitutive level of α_d transcription within a cell, as well as changes in the level of transcription in response to internal or external agents. Identification of agents which modify transcription and/or translation of α_d can, in turn, be assessed for potential therapeutic or prophylactic value. DNA of the invention also makes possible *in situ* hybridization of α_d DNA to cellular RNA to determine the cellular localization of α_d specific messages within complex cell populations and tissues.

DNA of the invention is also useful for identification of non-human polynucleotide sequences which display homology to human α_d sequences. Possession of non-human α_d DNA sequences permits development of animal models (including, for example, transgenic models) of the human system.

transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and an activating domain, expressing in the host cells a first hybrid DNA sequence encoding a first fusion of part or all of α_d and either the DNA binding domain or the activating domain of the transcription factor, expressing in the host cells a library of second hybrid DNA sequences encoding second fusions of part or all of putative α_d binding proteins and the DNA binding domain or activating domain of the transcription factor which is not incorporated in the first fusion, detecting binding of an α_d binding protein to α_d in a particular host cell by detecting the production of reporter gene product in the host cell, and isolating second hybrid DNA sequences encoding α_d binding protein from the particular host cell.

Hybridoma cell lines which produce antibodies specific for α_d are also comprehended by the invention. Techniques for producing hybridomas which secrete monoclonal antibodies are well known in the art. Hybridoma cell lines may be generated after immunizing an animal with purified α_d, variants of α_d or cells which express α_d or a variant thereof on the extracellular membrane surface. Immunogen cell types include cells which express α_d *in vivo*, or transfected prokaryotic or eukaryotic cell lines which normally do not normally express α_d *in vivo*.

The value of the information contributed through the disclosure of the DNA and amino acid sequences of α_d is manifest. In one series of examples, the disclosed α_d CDNA sequence makes possible the isolation of the human α_d genomic DNA sequence, including transcriptional control elements for the genomic sequence. Identification of α_d allelic variants and heterologous species (*e.g.*, rat or mouse) DNAs is also comprehended. Isolation of the human α_d genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of the α_d cDNA sequence as a probe to screen an appropriate

thereof on a solid support coated (or impregnated with) a fluorescent agent, labelling the ligand with a compound capable of exciting the fluorescent agent, contacting the immobilized α_d with the labelled ligand in the presence and absence of a putative modulator compound, detecting light emission by the fluorescent agent, and identifying modulating compounds as those compounds that affect the emission of light by the fluorescent agent in comparison to the emission of light by the fluorescent agent in the absence of a modulating compound. Alternatively, the α_d ligand may be immobilized and α_d may be labelled in the assay.

Yet another method contemplated by the invention for identifying compounds that modulate the interaction between α_d and a ligand involves transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and an activating domain, expressing in the host cells a first hybrid DNA sequence encoding a first fusion of part or all of α_d and either the DNA binding domain or the activating domain of the transcription factor, expressing in the host cells a second hybrid DNA sequence encoding part or all of the ligand and the DNA binding domain or activating domain of the transcription factor which is not incorporated in the first fusion, evaluating the effect of a putative modulating compound on the interaction between α_d and the ligand by detecting binding of the ligand to α_d in a particular host cell by measuring the production of reporter gene product in the host cell in the presence or absence of the putative modulator, and identifying modulating compounds as those compounds altering production of the reported gene product in comparison to production of the reporter gene product in the absence of the modulating compound. Presently preferred for use in the assay are the *lexA* promoter, the *lexA* DNA binding domain, the GAL4 transactivation domain, the *lacZ* reporter gene, and a yeast host cell.

A modified version of the foregoing assay may be used in isolating ucleotide encoding a protein that binds to α_d by transforming or

function. Fusion polypeptides are also provided, wherein α_d amino acid sequences are expressed contiguously with amino acid sequences from other polypeptides. Such fusion polypeptides may possess modified biological, biochemical, and/or immunological properties in comparison to wild-type α_d. Analog polypeptides including additional amino acid (*e.g.*, lysine or cysteine) residues that facilitate multimer formation are contemplated.

Also comprehended by the present invention are polypeptides and other non-peptide molecules which specifically bind to α_d. Preferred binding molecules include antibodies (*e.g.*, monoclonal and polyclonal antibodies), counterreceptors (*e.g.*, membrane-associated and soluble forms) and other ligands (*e.g.*, naturally occurring or synthetic molecules), including those which competitively bind α_d in the presence of α_d monoclonal antibodies and/or specific counterreceptors. Binding molecules are useful for purification of α_d polypeptides and identifying cell types which express α_d. Binding molecules are also useful for modulating (*i.e.*, inhibiting, blocking or stimulating) of *in vivo* binding and/or signal transduction activities of α_d.

Assays to identify α_d binding molecules are also provided, including immobilized ligand binding assays, solution binding assays, scintillation proximity assays, di-hybrid screening assays, and the like.

In vitro assays for identifying antibodies or other compounds that modulate the activity of α_d may involve, for example, immobilizing α_d or a natural ligand to which α_d binds, detectably labelling the nonimmobilized binding partner, incubating the binding partners together and determining the effect of a test compound on the amount of label bound wherein a reduction in the label bound in the presence of the test compound compared to the amount of label bound in the absence of the test compound indicates that the test agent is an inhibitor of α_d binding.

Another type of assay for identifying compounds that modulate the interaction between α_d and a ligand involves immobilizing α_d or a fragment

As another aspect of the invention, monoclonal or polyclonal antibodies specific for α_d may be employed in immunohistochemical analysis to localize α_d to subcellular compartments or individual cells within tissues. Immunohistochemical analyses of this type are particularly useful when used in combination with *in situ* hybridization to localize both α_d mRNA and polypeptide products of the α_d gene.

Identification of cell types which express α_d may have significant ramifications for development of therapeutic and prophylactic agents. It is anticipated that the products of the invention related to α_d can be employed in the treatment of diseases wherein macrophages are an essential element of the disease process. Animal models for many pathological conditions associated with macrophage activity have been described in the art. For example, in mice, macrophage recruitment to sites of both chronic and acute inflammation is reported by Jutila, *et al.*, *J.Leukocyte Biol. 54*:30-39 (1993). In rats, Adams, *et al.*, [*Transplantation 53*:1115-1119(1992) and *Transplantation 56*:794-799 (1993)] describe a model for graft arteriosclerosis following heterotropic abdominal cardiac allograft transplantation. Rosenfeld, *et al.*, [*Arteriosclerosis 7*:9-23 (1987) and *Arteriosclerosis 7*:24-34 (1987)] describe induced atherosclerosis in rabbits fed a cholesterol supplemented diet. Hanenberg, *et al.*, [*Diabetologia 32*:126-134 (1989)] report the spontaneous development of insulin-dependent diabetes in BB rats. Yamada *et al.*, [*Gastroenterolgy 104*:759-771 (1993)] describe an induced inflammatory bowel disease, chronic granulomatous colitis, in rats following injections of streptococcal peptidoglycan-polysaccharide polymers. Cromartie, *et al.*, [*J.Exp.Med. 146*:1585-1602 (1977)] and Schwab, *et al.*, [*Infection and Immunity 59*:4436-4442 (1991)] report that injection of streptococcal cell wall protein into rats results in an arthritic condition characterized by inflammation of peripheral joints and subsequent joint destruction. Finally, Huitinga, *et al.*, [*Eur.J.Immunol 23*:709-715 (1993) describe experimental allergic encephalomyelitis, a model for multiple sclerosis, in Lewis rats. In each of these

models, α_d antibodies, other α_d binding proteins, or soluble forms of α_d are utilized to attenuate the disease state, presumably through inactivation of macrophage activity.

Pharmaceutical compositions for treatment of these and other disease states are provided by the invention. Pharmaceutical compositions are designed for the purpose of inhibiting interaction between α_d and its ligand(s) and include various soluble and membrane-associated forms of α_d (comprising the entire α_d polypeptide, or fragments thereof which actively participate in α_d binding), soluble and membrane-associated forms of α_d binding proteins (including antibodies, ligands, and the like), intracellular or extracellular modulators of α_d binding activity, and/or modulators of α_d and/or α_d-ligand polypeptide expression, including modulators of transcription, translation, post-translational processing and/or intracellular transport. The invention also comprehends methods for treatment of disease states in which α_d binding is implicated, wherein a patient suffering from said disease state is provided an amount of a pharmaceutical composition of the invention sufficient to modulate levels of α_d binding. The method of treatment of the invention is applicable to disease states such as, but not limited to, Type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, and rheumatoid arthritis.

Brief Description of the Drawing

Numerous other aspects and advantages of the present invention will be apparent upon consideration of the following description thereof, reference being made to the drawing wherein:

Figure 1A through 1D comprises an alignment of the human amino acid sequences of CD11b (SEQ ID NO: 3), CD11c (SEQ ID NO: 4) and α_d (SEQ ID NO: 2).

Detailed Description of the Invention

The present invention is illustrated by the following examples relating to the isolation of a cDNA clone encoding α_d from a human spleen cDNA library. More particularly, Example 1 illustrates the use of anti-canine α_{TM1} antibody in an attempt to detect a homologous human protein. Example 2 details purification of canine α_{TM1} and N-terminal sequencing of the polypeptide to design oligonucleotide primers for PCR amplification of the canine α_{TM1} gene. Example 3 addresses large scale purification of canine α_{TM1} for internal sequencing in order to design additional PCR primers. Example 4 describes use of the PCR and internal sequence primers to amplify a fragment of the canine α_{TM1} gene. Example 5 addresses cloning of the human α_d-encoding cDNA sequence. Example 6 describes Northern blot hybridization analysis of human tissues and cells for expression of α_d mRNA. Example 7 details the construction of human α_d expression plasmids and transfection of COS cells with the resulting plasmids. Example 8 addresses ELISA analysis of α_d expression in transfected COS cells. Example 9 describes FACS analysis of COS cells transfected with human α_d expression plasmids. Example 10 addresses immunoprecipitation of CD18 in association with α_d in co-transfected COS cells. Example 11 relates to stable transfection of α_d expression constructs in Chinese hamster ovary cells. Example 12 addresses CD18-dependent binding of α_d to the intercellular adhesion molecule, ICAM-R. Example 13 describes scintillation proximity screening assays to identify inhibitors of α_d ligand/anti-ligand binding interactions. Example 14 addresses construction of expression plasmids which encode soluble forms of α_d. Example 15 relates to production of α_d-specific monoclonal antibodies. Example 16 describes analysis of α_d tissue distribution using polyclonal antiserum. Example 17 describes isolation of rat cDNA sequences which show homology to human α_d gene sequences. Example 18 relates to construction of rat α_d I domain expression plasmids, including I domain/IgG fusion proteins, and production of monoclonal antibodies to I domain fusion

proteins. Example 19 addresses isolation of mouse cDNA sequences which show homology to human α_d gene sequences. Example 20 describes isolation of additional mouse α_d cDNA clones used for conformational sequence analysis. Example 21 relates to *in situ* hybridization analysis of various mouse tissues to determine tissue and cell specific expression of the putative mouse homolog to human α_d. Example 22 describes generation of expression constructs which encode the putative mouse homolog of human α_d. Example 23 addresses design of a "knock-out" mouse wherein the gene encoding the putative mouse homolog of human α_d is disrupted. Example 24 describes isolation of rabbit cDNA clones which show homology to human α_d encoding sequences. Example 25 describes animal models which resemble human disease states wherein modulation of α_d is assayed for therapeutic capabilities.

Example 1

Attempt to Detect a Human Homolog of Canine α_{TM1}

The monoclonal antibody Ca11.8H2 [Moore, et al., *supra*] specific for canine α_{TM1} was tested for cross-reactivity on human peripheral blood leukocytes in an attempt to identify a human homolog of canine α_{TM1}. Cell preparations (typically 1 x 10^6 cells) were incubated with undiluted hybridoma supernatant or a purified mouse IgG-negative control antibody (10 μg/ml) on ice in the presence of 0.1% sodium azide. Monoclonal antibody binding was detected by subsequent incubation with FITC-conjugated horse anti-mouse IgG (Vector Laboratories, Burlingame, CA) at 6 μg/ml. Stained cells were fixed with 2% w/v paraformaldehyde in phosphate buffered saline (PBS) and were analyzed with a Facstar Plus fluorescence-activated cell sorter (Becton Dickinson, Mountain View, CA). Typically, 10,000 cells were analyzed using logarithmic amplification for fluorescence intensity.

The results indicated that Ca11.8H2 did not cross-react with surface proteins expressed on human peripheral blood leukocytes, while the control cells,

neoplastic canine peripheral blood lymphocytes, were essentially all positive for α_{TM1}.

Because the monoclonal antibody Ca11.8H2 specific for the canine α subunit did not cross react with a human homolog, isolation of canine α_{TM1} DNA was deemed a necessary prerequisite to isolate a counterpart human gene if one existed.

Example 2

Affinity Purification Of Canine α_{TM1} For N-Terminal Sequencing

Canine α_{TM1} was affinity purified in order to determine N-terminal amino acid sequences for oligonucleotide probe/primer design. Briefly, anti-α_{TM1} monoclonal antibody Ca11.8H2 was coupled to Affigel 10 chromatographic resin (BioRad, Hercules, CA) and protein was isolated by specific antibody-protein interaction. Antibody was conjugated to the resin, according to the BioRad suggested protocol, at a concentration of approximately 5 mg antibody per ml of resin. Following the conjugation reaction, excess antibody was removed and the resin blocked with three volumes of 0.1 M ethanolamine. The resin was then washed with thirty column volumes of phosphate buffered saline (PBS).

Twenty-five grams of a single dog spleen were homogenized in 250 ml of buffer containing 0.32 M sucrose in 25 mM Tris-HCl, Ph 8.0, with protease inhibitors. Nuclei and cellular debris were pelleted with centrifugation at 1000 g for 15 minutes. Membranes were pelleted from the supernatant with centrifugation at 100,000 g for 30 minutes. The membrane pellet was resuspended in 200 ml lysis buffer (50 mM NaCl, 50 mM borate, pH 8.0, with 2% NP-40) and incubated for 1 hour on ice. Insoluble material was then pelleted by centrifugation at 100,000 g for 60 minutes. Ten milliliters of the cleared lysate were transferred to a 15 ml polypropylene tube with 0.5 ml Ca11.8H2-conjugated Affigel 10 resin described above. The tube was incubated overnight at 4°C with rotation and the resin subsequently washed with 50 column volumes

D-PBS. The resin was then transferred to a microfuge tube and boiled for ten minutes in 1 ml Laemmli (non-reducing) sample buffer containing 0.1 M Tris-HCl, pH 6.8, 2% SDS, 20% glycerol and 0.002% bromophenol blue. The resin was pelleted by centrifugation and discarded; the supernatant was treated with 1/15 volume β-mercaptoethanol (Sigma, St. Louis, MO) and run on a 7% polyacrylamide gel. The separated proteins were transferred to Immobilon PVDF membrane (Millipore, Bedford, MA) as follows.

The gels were washed once in deionized, Millipore-filtered water and equilibrated for 15-45 minutes in 10 mM 3-[cyclohexylamino]-1-propanesulfonic acid (CAPS) transfer buffer, pH 10.5, with 10% methanol. Immobilon membranes were moistened with methanol, rinsed with filtered water, and equilibrated for 15-30 minutes in CAPS transfer buffer. The initial transfer was carried out using a Biorad transfer apparatus at 70 volts for 3 hours. The Immobilon membrane was removed after transfer and stained in filtered 0.1% R250 Coomassie stain for 10 minutes. Membranes were destained in 50% methanol/10% acetic acid three times, ten minutes each time. After destaining, the membranes were washed in filtered water and air-dried.

Protein bands of approximately 150 kD, 95 kD, 50 kD and 30 kD were detected. Presumably the 50 kD and 30 kD bands resulted from antibody contamination. N-terminal sequencing was then attempted on both the 150 kD and 95 kD bands, but the 95 kD protein was blocked, preventing sequencing. The protein band of 150 kD was excised from the membrane and directly sequenced with an Applied Biosystems (Foster City, CA) Model 473A protein sequencer according to the manufacturer's instructions. The resulting amino acid sequence is set in SEQ ID NO: 5 using single letter amino acid designations.

FNLDVEEPMVFQ (SEQ ID NO: 5)

The identified sequence included the FNLD sequence characteristic of α subunits of the integrin family [Tamura, *et al.*, *J.Cell.Biol. 111*:1593-1604 (1990)].

Primer Design and Attempt to Amplify Canine α_{TM1} Sequences

From the N-terminal sequence information, three oligonucleotide probes were designed for hybridization: a) "Tommer," a fully degenerate oligonucleotide; b) "Patmer," a partially degenerate oligonucleotide; and c) "Guessmer," a nondegenerate oligonucleotide based on mammalian codon usage. These probes are set out below as SEQ ID NOS: 6, 7 and 8, respectively. Nucleic acid symbols are in accordance with 37 C.F.R. §1.882 for these and all other nucleotide sequences herein.

5´-TTYAAYYTGGAYGTNGARGARCCNATGGTNTTYCA-3´ (SEQ ID NO: 6)
5´-TTCAACCTGGACGTGGAGGAGCCCATGGTGTTCCAA-3´ (SEQ ID NO: 7)
5´-TTCAACCTGGACGTNGAASANCCCATGGTCTTCCAA-3´ (SEQ ID NO: 8)

Based on sequencing data, no relevant clones were detected using these oligonucleotides in several low stringency hybridizations to a canine spleen/peripheral blood macrophage cDNA library cloned into λZAP (Stratagene, La Jolla, CA).

Four other oligonucleotide primers, designated 5´Deg, 5´Spec, 3´Deg and 3´Spec (as set out in SEQ ID NOS: 9, 10, 11 and 12, respectively, wherein Deg indicates degenerate and Spec indicates non-degenerate) were subsequently designed based on the deduced N-terminal sequence for attempts to amplify canine α_{TM1} sequences by PCR from phage library DNA purified from plate lysates of the Stratagene library described above.

5´-TTYAAYYTNGAYGTNGARGARCC-3´ (SEQ ID NO: 9)
5´-TTYAAYYTGGACGTNGAAGA-3´ (SEQ ID NO: 10)

5′-TGRAANACCATNGGYTC-3′ (SEQ ID NO: 11)

5′-TTGGAAGACCATNGGYTC-3′ (SEQ ID NO: 12)

The α_{TM1} oligonucleotide primers were paired with T3 or T7 vector primers, as set out in SEQ ID NOS: 13 and 14, respectively, which hybridize to sequences flanking the polylinker region in the Bluescript phagemid found in λZAP.

5′-ATTAACCCTCACTAAAG-3′ (SEQ ID NO: 13)

5′-AATACGACTCACTATAG-3′ (SEQ ID NO: 14)

The PCR amplification was carried out in *Taq* buffer (Boehringer Mannheim, Indianapolis, IN) containing magnesium with 150 ng of library DNA, 1 μg of each primer, 200 μM dNTPs and 2.5 units *Taq* polymerase (Boehringer Mannheim) and the products were separated by electrophoresis on a 1% agarose gel in Tris-Acetate-EDTA (TAE) buffer with 0.25 μg/ml ethidium bromide. DNA was transferred to a Hybond (Amersham, Arlington Heights, IL) membrane by wicking overnight in 10X SSPE. After transfer, the immobilized DNA was denatured with 0.5 M NaOH with 0.6 M NaCl, neutralized with 1.0 M Tris-HCl, pH 8.0, in 1.5 M NaCl, and washed with 2X SSPE before UV crosslinking with a Stratalinker (Stratagene) crosslinking apparatus. The membrane was incubated in prehybridization buffer (5X SSPE, 4X Denhardts, 0.8% SDS, 30% formamide) for 2 hr at 50°C with agitation.

Oligonucleotide probes 5′Deg, 5′Spec, 3′Deg and 3′Spec (SEQ ID NOS: 9, 10, 11 and 12, respectively) were labeled using a Boehringer Mannheim kinase buffer with 100-300 μCi γP^{32}-dATP and 1-3 units of polynucleotide kinase for 1-3 hr at 37°C. Unincorporated label was removed with Sephadex G-25 fine (Pharmacia, Piscataway, NJ) chromatography using 10 mM Tris-HCl, pH 8.0, 1 mM EDTA (TE) buffer and the flow-through added directly to the prehybridization solution. Membranes were probed for 16 hr at 42°C with

agitation and washed repeatedly, with a final stringency wash of 1X SSPE/0.1% SDS at 50° for 15 min. The blot was then exposed to Kodak X-Omat AR film for 1-4 hours at -80°C.

The oligonucleotides 5´Deg, 5´Spec, 3´Deg and 3´Spec only hybridized to PCR products from the reactions in which they were used as primers and failed to hybridize as expected to PCR products from the reactions in which they were not used as primers. Thus, it was concluded that none of the PCR products were specific for α_{TM1} because no product hybridized with all of the appropriate probes.

Example 3

Large Scale Affinity Purification Of Canine α_{TM1} For Internal Sequencing

In order to provide additional amino acid sequence for primer design, canine α_{TM1} was purified for internal sequencing. Three sections of frozen spleen (approximately 50 g each) and frozen cells from two partial spleens from adult dogs were used to generate protein for internal sequencing. Fifty grams of spleen were homogenized in 200-300 ml borate buffer with a Waring blender. The homogenized material was diluted with 1 volume of buffer containing 4% NP-40, and the mixture then gently agitated for at least one hour. The resulting lysate was cleared of large debris by centrifugation at 2000 g for 20 min, and then filtered through either a Corning (Corning, NY) prefilter or a Corning 0.8 micron filter. The lysate was further clarified by filtration through the Corning 0.4 micron filter system.

Splenic lysate and the antibody-conjugated Affigel 10 resin described in Example 2 were combined at a 150:1 volume ratio in 100 ml aliquots and incubated overnight at 4°C with rocking. The lysate was removed after centrifugation at 1000 g for 5 minutes, combined with more antibody-conjugated Affigel 10 resin and incubated overnight as above. The absorbed resin aliquots were then combined and washed with 50 volumes D-PBS/0.1% Tween 20 and the

resin transferred to a 50 ml Biorad column. Adsorbed protein was eluted from the resin with 3-5 volumes of 0.1 M glycine (pH 2.5); fractions of approximately 900 μl were collected and neutralized with 100 μl 1 M Tris buffer, pH 8.0. Aliquots of 15 μl were removed from each fraction and boiled in an equal volume of 2X Laemmli sample buffer with 1/15 volume 1 M dithiothreitol (DTT). These samples were electrophoresed on 8% Novex (San Diego, CA) polyacrylamide gels and visualized either by Coomassie stain or by silver stain using a Daiichi kit (Enprotech, Natick, MA) according to the manufacturer's suggested protocol. Fractions which contained the largest amounts of protein were combined and concentrated by vacuum. The remaining solution was diluted by 50% with reducing Laemmli sample buffer and run on 1.5 mm 7% polyacrylamide gels in Tris-glycine/SDS buffer. Protein was transferred from the gels to Immobilon membrane by the procedure described in Example 2 using the Hoefer transfer apparatus.

The protein bands corresponding to canine α_{TM1} were excised from 10 PVDF membranes and resulted in approximately 47 μg total protein. The bands were destained in 4 ml 50% methanol for 5 minutes, air dried and cut into 1 x 2 mm pieces. The membrane pieces were submerged in 2 ml 95% acetone at 4°C for 30 minutes with occasional vortexing and then air dried.

Prior to proteolytic cleavage of the membrane bound protein, 3 mg of cyanogen bromide (CNBr) (Pierce, Rockford, IL) were dissolved in 1.25 ml 70% formic acid. This solution was then added to a tube containing the PVDF membrane pieces and the tube incubated in the dark at room temperature for 24 hours. The supernatant (S1) was then removed to another tube and the membrane pieces washed with 0.25 ml 70% formic acid. This supernatant (S2) was removed and added to the previous supernatant (S1). Two milliliters of Milli Q water were added to the combined supernatants (S1 and S2) and the solution lyophilized. The PVDF membrane pieces were dried under nitrogen and extracted again with 1.25 ml 60% acetonitrile, 0.1% tetrafluoroacetic acid (TFA) at 42°C for 17 hours.

This supernatant (S3) was removed and the membrane pieces extracted again with 1.0 ml 80% acetonitrile with 0.08% TFA at 42°C for 1 hour. This supernatant (S4) was combined with the previous supernatants (S1, S2 and S3) and vacuum dried.

The dried CNBr fragments were then dissolved in 63 μl 8 M urea, 0.4 M NH_4HCO_3. The fragments were reduced in 5 μl 45 mM dithiothreitol (DTT) and subsequently incubated at 50°C for 15 minutes. The solution was then cooled to room temperature and the fragments alkylated by adding 5 μl 100 mM iodoacetamide (Sigma, St. Louis, MO). Following a 15 minute incubation at room temperature, the sample was diluted with 187 μl Milli Q water to a final urea concentration of 2.0 M. Trypsin (Worthington, Freehold, NJ) was then added at a ratio of 1:25 (w:w) of enzyme to protein and the protein digested for 24 hours at 37°C. Digestion was terminated with addition of 30 μl TFA.

The protein fragments were then separated with high performance liquid chromatography (HPLC) on a Waters 625 LC system (Millipore, Milford, MA) using a 2.1 x 250 mm, 5 micron Vydac C-18 column (Vydac, Hesperia, CA) equilibrated in 0.05% TFA and HPLC water (buffer A). The peptides were eluted with increasing concentration of 80% acetonitrile in 0.04% TFA (buffer B) with a gradient of 38-75% buffer B for 65-95 minutes and 75-98% buffer B for 95-105 minutes. Peptides were fractionated at a flow rate of 0.2 ml/minute and detected at 210 nm.

Following fractionation, the amino acid sequence of the peptides was analyzed by automated Edman degradation performed on an Applied Biosystems Model 437A protein sequencer using the manufacturer's standard cycles and the Model 610A Data Analysis software program, Version 1.2.1. All sequencing reagents were supplied by Applied Biosystems. The amino acid sequences of seven of the eight internal fragments are set out below wherein "X" indicates the identity of the amino acid was not certain.

VFQEXGAGFGQ	(SEQ ID NO: 15)
LYDXVAATGLXQPI	(SEQ ID NO: 16)
PLEYXDVIPQAE	(SEQ ID NO: 17)
FQEGFSXVLX	(SEQ ID NO: 18)
TSPTFIXMSQENVD	(SEQ ID NO: 19)
LVVGAPLEVVAVXQTGR	(SEQ ID NO: 20)
LDXKPXDTA	(SEQ ID NO: 21)

Primer Design

One internal amino acid sequence (set out in SEQ ID NO: 22) obtained was then used to design a fully degenerate oligonucleotide primer, designated p4(R) as set out in SEQ ID NO: 23.

FGEQFSE	(SEQ ID NO: 22)
5´-RAANCCYTCYTGRAAACTYTC-3´	(SEQ ID NO: 23)

Example 4

PCR Cloning Of A Canine α_{TM1} Fragment

The 5´ portion of the canine α_{TM1} gene was amplified from double-stranded canine splenic cDNA by PCR.

A. Generation of Double Stranded Canine Spleen cDNA

One gram of frozen material from a juvenile dog spleen was ground in liquid nitrogen on dry ice and homogenized in 20 ml RNA-Stat 60 buffer (Tel-Test B, Inc, Friendswood, TX). Four ml chloroform were added, and the solution extracted by centrifugation at 12,000 g for 15 minutes. RNA was precipitated from the aqueous layer with 10 ml ethanol. Poly A^+ RNA was then selected on Dynal Oligo dT Dynabeads (Dynal, Oslo, Norway). Five aliquots of 100 μg total RNA were combined and diluted with an equal volume of 2X binding

buffer (20 mM Tris-HCl, pH 7.5, 1.0 M LiCl, 1 mM EDTA, 0.1% SDS). RNA was then incubated 5 minutes with the Oligo dT Dynabeads (1.0 ml or 5 mg beads for all the samples). Beads were washed with buffer containing 10 mM Tris-HCl, pH 7.5, 0.15 M LiCl, 1 mM EDTA and 0.1% SDS, according to the manufacturer's suggested protocol prior to elution of poly A^+ mRNA with 2 mM EDTA, pH 7.5. Double-stranded cDNA was then generated using the eluted poly A^+ mRNA and the Boehringer Mannheim cDNA Synthesis Kit according to the manufacturer's suggested protocol.

B. Isolation of a Partial Canine α_{TM1} cDNA

Oligonucleotide primers 5'Deg (SEQ ID NO: 9) and p4(R) (SEQ ID NO: 23) were employed in a standard PCR reaction using 150 ng double-stranded cDNA, 500 ng of each primer, 200 μM dNTPs and 1.5 units *Taq* polymerase (Bochringer Mannheim) in *Taq* buffer (Boehringer Mannheim) with magnesium. The resulting products (1 μl of the original reaction) were subjected to a second round of PCR with the same primers to increase product yield. This band was eluted from a 1% agarose gel onto Schleicher & Schuell (Keene, NH) NA45 paper in a buffer containing 10 mM Tris-HCl, pH 8, 1 mM EDTA, 1.5 M NaCl at 65°C, precipitated, and ligated into the pCR™II vector (Invitrogen, San Diego, CA) using the TA cloning kit (Invitrogen) and the manufacturer's suggested protocol. The ligation mixture was transformed by electroporation into XL-1 Blue bacteria (Stratagene). One clone, 2.7, was determined to contain sequences corresponding to α_{TM1} peptide sequences which were not utilized in design of the primers.

Sequencing was performed with an Applied Biosystems 373A DNA sequencer (Foster City, CA) with a Dye-deoxy terminator cycle sequence kit (ABI) in which fluorescent-labeled dNTPs were incorporated in an asymmetric PCR reaction [McCabe, "Production of Single Stranded DNA by Asymmetric PCR," in PCR Protocols: A Guide to Methods and Applications, Innis, *et al.*

(eds.) pp. 76-83 Academic Press: New York (1990)] as follows. Samples were held at 96°C for 4 minutes and subjected to 25 cycles of the step sequence: 96°C, for 15 seconds; 50°C for 1 second; 60°C for 4 minutes. Sequence data was automatically down-loaded into sample files on the computer that included chromatogram and text files. The sequence of the entire insert of clone 2.7 is set out in SEQ ID NO: 24.

Attempts to isolate the full length canine α_{TM1} cDNA from the Stratagene library (as described in Example 2) were unsuccessful. Approximately 1 x 10^6 phage plaques were screened by hybridization under low stringency conditions using 30% formamide with clone 2.7 as a probe, but no positive clones resulted. Attempts to amplify relevant sequences downstream from those represented in clone 2.7 using specific oligonucleotides derived from clone 2.7 or degenerate primers based on amino acid sequence from other peptide fragments paired with a degenerate oligonucleotide based on the conserved α subunit amino acid motif GFFKR [Tamura, *et al., supra*] were also unsuccessful.

Example 5

Cloning Of A Putative Human Homolog Of Canine α_{TM1}

To attempt the isolation of a human sequence homologous to canine α_{TM1} the approximately 1 kb canine α_{TM1} fragment from clone 2.7 was used as a probe. The probe was generated by PCR under conditions described in Example 2 using NT2 (as set out in SEQ ID NO: 25) and p4(R) (SEQ ID NO: 23) primers.

5´-GTNTTYCARGARGAYGG-3´ (SEQ ID NO: 25)

The PCR product was purified using the Qiagen (Chatsworth, GA) Quick Spin kit and the manufacturer's suggested protocol. The purified DNA (200 ng) was labeled with 200 μCi α^{32}PdCTP using the Boehringer Mannheim Random Prime

Labelling kit and the manufacturer's suggested protocol. Unincorporated isotope was removed with Sephadex G25 (fine) gravity chromatography. The probe was denatured with 0.2 N NaOH and neutralized with 0.4 M Tris-HCl, pH 8.0, before use.

Colony lifts on Hybond filters (Amersham) of a human spleen cDNA library in pCDNA/Amp (Invitrogen, San Diego, CA) were prepared. The filters were initially denatured and neutralized as described in Example 2 and subsequently incubated in a prehybridization solution (8 ml/filter) with 30% formamide at 50°C with gentle agitation for 2 hours. Labeled probe as described above was added to this solution and incubated with the filters for 14 hours at 42°C. The filters were washed twice in 2X SSC/0.1% SDS at 37°C and twice in 2X SSC/0.1% SDS at 50°C. Final stringency washes were 1X SSC/0.1% SDS, twice at 65°C (1X SSC is 150 mM NaCl, 15 mM sodium citrate, pH 7.0). Filters were exposed to Kodak X-Omat AR film for six hours with an intensifying screen. Colonies giving signals on duplicate lifts were streaked on LB medium with magnesium (LBM)/carbenicillin plates and incubated overnight at 37°C. Resulting streaked colonies were lifted with Hybond filters and these filters were treated as above. The filters were hybridized under more stringent conditions with the 1 kb probe from clone 2.7, labeled as previously described, in a 50% formamide hybridization solution at 50°C for 3 hours. Probed filters were washed with a final stringency of 0.1 X SSC/0.1% SDS at 65°C and exposed to Kodak X-Omat AR film for 2.5 hours at -80°C with an intensifying screen. Positive colonies were identified and cultured in LBM/carbenicillin medium overnight. DNA from the cultures was prepared using the Promega Wizard miniprep kit according to the manufacturer's suggested protocol and the resulting DNA was sequenced.

The initial screening resulted in 18 positive clones, while the secondary screening under more stringent hybridization conditions produced one positive clone which was designated 19A2. The DNA and deduced amino acid

sequences of the human α_d clone 19A2 are set out in SEQ ID NOS: 1 and 2, respectively.

Characteristics Of The Human α_d cDNA and Predicted Polypeptide

Clone 19A2 encompasses the entire coding region for the mature protein, plus 48 bases (16 amino acid residues) of the 5′ upstream signal sequence and 241 bases of 3′ untranslated sequence which do not terminate in a polyadenylation sequence. The core molecular weight of the mature protein is predicted to be around 125 kD. The extracellular domain is predicted to encompass approximately amino acid residues 17 through 1108 of SEQ ID NO: 2. This extracellular region is contiguous with about a 20 amino acid region homologous to the human CD11c transmembrane region (residues 1109 through 1128 of SEQ ID NO: 2). The cytoplasmic domain comprises approximately 30 amino acids (about residues 1129 through 1161 of SEQ ID NO: 2). The protein also contains a region (around residues 150 through 352) of approximately 202 amino acids homologous to the I (insertion) domain common to CD11a, CD11b and CD11c [Larson and Springer, *supra*], α_E [Shaw, *et al., J.Biol.Chem. 269*:6016-6025 (1994)] and in VLA-1 and VLA-2, [Tamura, *et al., supra*]. The I domain in other integrins has been shown to participate in ICAM binding [Landis, *et al., J.Cell.Biol. 120*:1519-1527 (1993); Diamond, *et al., J.Cell.Biol. 120*:1031-1043 (1993)], suggesting that α_d may also bind members of the ICAM family of surface molecules. This region has not been demonstrated to exist in any other integrin subunits.

The deduced amino acid sequence of α_d shows approximately 36% identity to that of CD11a, approximately 60% identity to CD11b and approximately 66% identity to CD11c. An alignment of amino acid sequences for (CD11b SEQ ID NO: 3), CD11c (SEQ ID NO: 4) and α_d (SEQ ID NO: 2) is presented in Figure 1.

The cytoplasmic domains of α subunits in β_2 integrins are typically distinct from one another within the same species, while individual α subunits show high degrees of homology across species boundaries. Consistent with these observations, the cytoplasmic region of α_d differs markedly from CD11a, CD11b, and CD11c except for a membrane proximal GFFKR amino acid sequence which has been shown to be conserved among all α integrins [Rojiani, *et al.*, *Biochemistry 30*: 9859-9866 (1991)]. Since the cytoplasmic tail region of integrins has been implicated in "inside out" signaling and in avidity regulation [Landis *et al.*, *supra*], it is possible that α_d interacts with cytosolic molecules distinct from those interacting with CD11a, CD11b, and CD11c, and, as a result, participates in signaling pathways distinct from those involving other β_2 integrins.

The extracellular domain of α_d contains a conserved DGSGS amino acid sequence adjacent the I-domain; in CD11b, the DGSGS sequence is a metal-binding region required for ligand interaction [Michishita, *et al. Cell* 72:857-867 (1993)]. Three additional putative cation binding sites in CD11b and CD11c are conserved in the α_d sequence at amino acids 465-474, 518-527, and 592-600 in clone 19A2 (SEQ ID NO: 1). The α_d I-domain is 36%, 62%, and 57% identical to the corresponding regions in CD11a, CD11b, and CD11c, respectively, and the relatively low sequence homology in this region suggests that α_d may interact with a set of extracellular proteins distinct from proteins with which other known β_2 integrins interact. Alternatively, the affinity of α_d for known β_2 integrin ligands, for example, ICAM-1, ICAM-2 and/or ICAM-R, may be distinct from that demonstrated for the other β_2 integrin/ICAM interactions. [See Example 12.]

Example 6

Northern Analysis of Human α_d Expression in Tissues

In order to determine the relative level of expression and tissue specificity of α_d, Northern analysis was performed using fragments from clone 19A2 as probes. Approximately 10 μg of total RNA from each of several human tissues or cultured cell lines were loaded on a formaldehyde agarose gel in the presence of 1 μg of ethidium bromide. After electrophoresis at 100 V for 4 hr, the RNA was transferred to a nitrocellulose membrane (Schleicher & Schuell) by wicking in 10X SSC overnight. The membrane was baked 1.5 hr at 80°C under vacuum. Prehybridization solution containing 50% formamide in 3-(N-morpholino)propane sulfonic acid (MOPS) buffer was used to block the membrane for 3 hr at 42°C. Fragments of clone 19A2 were labeled with the Boehringer Mannheim Random Prime kit according to the manufacturer's instructions including both αP^{32}dCTP and αP^{32}dTTP. Unincorporated label was removed on a Sephadex G25 column in TE buffer. The membrane was probed with 1.5×10^6 counts per ml of prehybridization buffer. The blot was then washed successively with 2X SSC/0.1% SDS at room temperature, 2X SSC/0.1% SDS at 42°C, 2X SSC/0.1% SDS at 50°C, 1X SSC/0.1% SDS at 50°C, 0.5X SSC/0.1% SDS at 50°C and 0.1X SSC/0.1% SDS at 50°C. The blot was then exposed to film for 19 hr.

Hybridization using a *Bst*XI fragment from clone 19A2 (corresponding to nucleotides 2011 to 3388 in SEQ ID NO: 1) revealed a weak signal in the approximately 5 kb range in liver, placenta, thymus, and tonsil total RNA. No signal was detected in kidney, brain or heart samples. The amount of RNA present in the kidney lane was minimal, as determined with ethidium bromide staining.

When using a second fragment of clone 19A2 (encompassing the region from bases 500 to 2100 in SEQ ID NO: 1), RNA transcripts of two different sizes were detected in a human multi-tissue Northern (MTN) blot using

polyA$^+$ RNA (Clontech). An approximately 6.5 kb band was observed in spleen and skeletal muscle, while a 4.5 kb band was detected in lung and peripheral blood leukocytes. The variation in sizes observed could be caused by tissue specific polyadenylation, cross reactivity of the probe with other integrin family members, or hybridization with alternatively spliced mRNAs.

Northern analysis using a third fragment from clone 19A2, spanning nucleotides 2000 to 3100 in SEQ ID NO: 1, gave results consistent with those using the other clone 19A2 fragments.

RNA from three myeloid lineage cell lines was also probed using the fragments corresponding to nucleotides 500 to 2100 and 2000 to 3100 in SEQ ID NO:1. A THP-1 cell line, previously stimulated with PMA, gave a diffuse signal in the same size range (approximately 5.0 kb), with a slightly stronger intensity than the tissue signals. RNA from unstimulated and DMSO-stimulated HL-60 cells hybridized with the α_d probe at the same intensity as the tissue samples, however, PMA treatment seemed to increase the signal intensity. Since PMA and DMSO drive HL-60 cell differentiation toward monocyte/macrophage and granulocyte pathways, respectively, this result suggests enhanced α_d expression in monocyte/macrophage cell types. U937 cells expressed the α_d message and this signal did not increase with PMA stimulation. No band was detected in Molt, Daudi, H9, JY, or Jurkat cells.

Example 7

Transient Expression of Human α_d Constructs

A. Generation of expression constructs

The human clone 19A2 lacks an initiating methionine codon and possibly some of the 5´ signal sequence. Therefore, in order to generate a human expression plasmid containing 19A2 sequences, two different strategies were used. In the first, two plasmids were constructed in which signal peptide sequences derived from genes encoding either CD11b or CD11c were spliced into clone

19A2 to generate a chimeric α_d sequence. In the second approach, a third plasmid was constructed in which an adenosine base was added at position 0 in clone 19A2 to encode an initiating methionine.

The three plasmids contained different regions which encoded the 5′ portion of the α_d sequence or the chimeric α_d sequence. The α_d region was PCR amplified (see conditions in Example 2) with a specific 3′ primer BamRev (set out below in SEQ ID NO: 26) and one of three 5′ primers. The three 5′ primers contained in sequence: (1) identical nonspecific bases at positions 1-6 allowing for digestion, an *Eco*RI site from positions 7-12 and a consensus Kozak sequence from positions 13-18; (2) a portion of the CD11b (primer ER1B) or CD11c (primer ER1C) signal sequence, or an adenosine (primer ER1D); and (3) an additional 15-17 bases specifically overlapping 5′ sequences from clone 19A2 to allow primer annealing. Primers ER1B, ER1C or ER1D are set out in SEQ ID NOS: 27, 28 or 29, respectively, where the initiating methionine codon is underlined and the *Eco*RI site is double underlined.

5′-CCACTGTCAGGATGCCCGTG-3′ (SEQ ID NO: 26)

5′-AGTTACGAATTCGCCACCATGGCTCTACGGGTGCTT(SEQ ID NO: 27)

5′-AGTTACGAATTCGCCACCATGACTCGGACTGTGCTT(SEQ ID NO: 28)

5′-AGTTACGAATTCGCCACCATGACCTTCGGCACTGTG(SEQ ID NO: 29)

The resulting PCR product was digested with *Eco*RI and *Bam*HI.

All three plasmids contained a common second α_d region (to be inserted immediately downstream from the 5′ region described in the previous paragraph) including the 3′ end of the α_d clone. The second α_d region, which

extended from nucleotide 625 into the *Xba*I site in the vector 3′ polylinker region of clone 19A2, was isolated by digestion of clone 19A2 with *Bam*HI and *Xba*I.

Three ligation reactions were prepared in which the 3′ α_d *Bam*HI/*Xba*I fragment was ligated to one of the three 5′ α_d *Eco*RI/*Bam*HI fragments using Boehringer Mannheim ligase buffer and T4 ligase (1 unit per reaction). After a 4 hour incubation at 14°C, an appropriate amount of vector pcDNA.3 (Invitrogen) digested with *Eco*RI and *Xba*I was added to each reaction with an additional unit of ligase. Reactions were allowed to continue for another 14 hours. One tenth of the reaction mixture was then transformed into competent XL-1 Blue cells. The resulting colonies were cultured and the DNA isolated as in Example 5. Digestion with *Eco*RI identified three clones which were positive for that restriction site, and thus, the engineered signal sequences. The clones were designated pATM.B1 (CD11b/α_d, from primer ER1B), pATM.C10 (CD11c/α_d, from primer ER1C) and pATM.D12 (adenosine/α_d from primer ER1d). The presence of the appropriate signal sequences in each clone was verified by nucleic acid sequencing.

B. Transfection of COS Cells

Expression from the α_d plasmids discussed above was effected by cotransfection of COS cells with the individual plasmids and a CD18 expression plasmid, pRC.CD18. As a positive control, COS cells were also co-transfected with the plasmid pRC.CD18 and a CD11a expression plasmid, pDC.CD11A.

Cells were passaged in culture medium (DMEM/10%FBS/pen-strep) into 10 cm Corning tissue culture-treated petri dishes at 50% confluency 16 hours prior to transfection. Cells were removed from the plates with Versene buffer (0.5 mM NaEDTA in PBS) without trypsin for all procedures. Before transfection, the plates were washed once with serum-free DMEM. Fifteen micrograms of each plasmid were added to 5 ml transfection buffer (DMEM with 20 μg/ml DEAE-Dextran and 0.5 mM chloroquine) on each plate. After 1.5

hours incubation at 37°C, the cells were shocked for 1 minute with 5 ml DMEM/10% DMSO. This DMSO solution was then replaced with 10 ml/plate culture medium.

Resulting transfectants were analyzed by ELISA, FACS, and immunoprecipitation as described in Examples 8, 9, and 10.

Example 8

ELISA Analysis of COS Transfectants

In order to determine if the COS cells co-transfected with CD18 expression plasmid pRC.CD18 and an α_d plasmid expressed α_d on the cell surface in association with CD18, ELISAs were performed using primary antibodies raised against CD18 (*e.g.*, TS1/18 purified from ATCC HB203). As a positive control, ELISAs were also performed on cells co-transfected with the CD18 expression plasmid and a CD11a expression plasmid, pDC.CD11A. The primary antibodies in this control included CD18 antibodies and anti-CD11a antibodies (*e.g.*, TS1/22 purified from ATCC HB202).

For ELISA, cells from each plate were removed with Versene buffer and transferred to a single 96-well flat-bottomed Corning tissue culture plate. Cells were allowed to incubate in culture media 2 days prior to assay. The plates were then washed twice with 150 μl/well D-PBS/0.5% teleost skin gelatin (Sigma) solution. This buffer was used in all steps except during the development. All washes and incubations were performed at room temperature. The wells were blocked with gelatin solution for 1 hour. Primary antibodies were diluted to 10 μg/ml in gelatin solution and 50 μl were then added to each well. Triplicate wells were set up for each primary antibody. After 1 hour incubation, plates were washed 3X with 150 μl/well gelatin solution. Secondary antibody (goat anti-mouse Ig/HRP-Fc specific [Jackson, West Grove, PA]) at a 1:3500 dilution was added at 50 μl/well and plates were incubated for 1 hour. After three washes, plates were developed for 20 minutes with 100 μl/well *o*-

phenyldiamine (OPD) (Sigma) solution (1 mg/ml OPD in citrate buffer) before addition of 50 μl/well 15% sulfuric acid.

Analysis of transfectants in the ELISA format with anti-CD18 specific antibodies revealed no significant expression above background in cells transfected only with the plasmid encoding CD18. Cells co-transfected with plasmid containing CD11a and CD18 showed an increase in expression over background when analyzed with CD18 specific antibodies or with reagents specific for CD11a. Further analysis of cells co-transfected with plasmids encoding CD18 and one of the α_d expression constructs (pATM.C10 or pATM.D12) revealed that cell surface expression of CD18 was rescued by concomitant expression of α_d. The increase in detectable CD18 expression in COS cells transfected with pATM.C10 or pATM.D12 was comparable to that observed in co-transfected CD11a/CD18 positive control cells.

Example 9

FACS Analysis of COS Transfectants

For FACS analysis, cells in petri dishes were fed with fresh culture medium the day after transfection and allowed to incubate 2 days prior to the assay. Transfectant cells were removed from the plates with 3 ml Versene, washed once with 5 ml FACS buffer (DMEM/2% FBS/0.2% sodium azide) and diluted to 500,000 cells/sample in 0.1 ml FACS buffer. Ten microliters of either 1 mg/ml FITC-conjugated CD18, CD11a, or CD11b specific antibodies (Becton Dickinson) or 800 μg/ml CFSE-conjugated murine 23F2G (anti-CD18) (ATCC HB11081) were added to each sample. Samples were then incubated on ice for 45 minutes, washed 3X with 5 ml/wash FACS buffer and resuspended in 0.2 ml FACS buffer. Samples were processed on a Becton Dickinson FACscan and the data analyzed using Lysys II software (Becton Dickinson).

COS cells transfected with CD18 sequences only did not stain for CD18, CD11a or CD11b. When co-transfected with CD11a/CD18, about 15%

of the cells stained with antibodies to CD11a or CD18. All cells transfected with CD18 and any α_d construct resulted in no detectable staining for CD11a and CD11b. The pATM.B1, pATM.C10 and pATM.D12 groups stained 4%, 13% and 8% positive for CD18, respectively. Fluorescence of the positive population in the CD11a/CD18 group was 4-fold higher than background. In comparison, the co-transfection of α_d constructs with the CD18 construct produced a positive population that showed a 4- to 7-fold increase in fluorescence intensity over background.

Example 10

Biotin-Labeled Immunoprecipitation of
Human α_d/CD18 Complexes from Co-transfected COS Cells

Immunoprecipitation was attempted on cells co-transfected with CD18 and each of the α_d expression plasmids separately described in Example 7 in order to determine if α_d could be isolated as part of the $\alpha\beta$ heterodimer complex characteristic of integrins.

Transfected cells (1-3 x 10^8 cells/group) were removed from petri dishes with Versene buffer and washed 3 times in 50 ml/group D-PBS. Each sample was labeled with 2 mg Sulpho-NHS Biotin (Pierce, Rockford, IL) for 15 minutes at room temperature. The reaction was quenched by washing 3 times in 50 ml/sample cold D-PBS. Washed cells were resuspended in 1 ml lysis buffer (1% NP40, 50 mM Tris-HCl, pH 8.0, 0.2 M NaCl, 2 mM Ca^{++}, 2 mM Mg^{++}, and protease inhibitors) and incubated 15 minutes on ice. Insoluble material was pelleted by centrifugation at 10,000 g for 5 minutes, and the supernatant removed to fresh tubes. In order to remove material non-specifically reactive with mouse immunoglobulin, a pre-clearance step was initially performed. Twenty-five micrograms of mouse immunoglobulin (Cappel, West Chester, PA) was incubated with supernatants at 4°C. After 2.5 hr, 100 μl (25 μg) rabbit anti-mouse Ig conjugated Sepharose (prepared from Protein A Sepharose 4B and rabbit anti-mouse IgG, both from Zymed, San Francisco, CA) was added to each sample;

incubation was continued at 4°C with rocking for 16 hours. Sepharose beads were removed from the supernatants by centrifugation. After pre-clearance, the supernatants were then treated with 20 μg anti-CD18 antibody (TS1.18) for 2 hours at 4°C. Antibody/antigen complexes were isolated from supernatants by incubation with 100 μl/sample rabbit anti-mouse/Protein A-sepharose preparation described above. Beads were washed 4 times with 10 mM HEPES, 0.2 M NaCl, and 1% Triton-X 100. Washed beads were pelleted and boiled for 10 minutes in 20 μl 2X Laemmli sample buffer with 2% β-mercaptoethanol. Samples were centrifuged and run on an 8% prepoured Novex polyacrylamide gel (Novex) at 100 V for 30 minutes. Protein was transferred to nitrocellulose membranes (Schleicher & Schuell) in TBS-T buffer at 200 mAmps for 1 hour. Membranes were blocked for 2 hr with 3% BSA in TBS-T. Membranes were treated with 1:6000 dilution of Strep-avidin horse radish peroxidase (POD) (Boehringer Mannheim) for 1 hour, followed by 3 washes in TBS-T. The Amersham Enhanced Chemiluminescence kit was then used according to the manufacturer's instructions to develop the blot. The membrane was exposed to Hyperfilm MP (Amersham) for 0.5 to 2 minutes.

Immunoprecipitation of CD18 complexes from cells transfected with pRC.CD18 and either pATM.B1, pATM.C10 or pATM.D12 revealed surface expression of a heterodimeric species consisting of approximately 100 kD β chain, consistent with the predicted size of CD18, and an α chain of approximately 150 kD, corresponding to α_d.

Example 11

Stable Transfection of Human α_d in Chinese Hamster Ovary Cells

To determine whether α_d is expressed on the cell surface as a heterodimer in association with CD18, cDNAs encoding each chain were both transiently and stably transfected into a cell line lacking both α_d and CD18.

For these experiments, α_d cDNA was augmented with additional leader sequences and a Kozak consensus sequence, as described in Example 7, and subcloned into expression vector pcDNA3. The final construct, designated pATM.D12, was co-transfected with a modified commercial vector, pDC1.CD18 encoding human CD18 into dihydrofolate reductase (DHFR)$^-$ Chinese hamster ovary (CHO) cells. The plasmid pDC1.CD18 encodes a DHFR$^+$ marker and transfectants can be selected using an appropriate nucleoside-deficient medium. The modifications which resulted in pDC1.CD18 are as follows.

The plasmid pRC/CMV (Invitrogen) is a mammalian expression vector with a cytomegalovirus promoter and ampicillin resistance marker gene. A DHFR gene from the plasmid pSC1190-DHFR was inserted into pRC/CMV 5′ of the SV40 origin of replication. In addition, a polylinker from the 5′ region of the plasmid pHF2G-DHF was ligated into the pRC/CMV/DHFR construct, 3′ to the DHFR gene. CD18 encoding sequences are subsequently cloned into the resulting plasmid between the 5′ flanking polylinker region and the bovine growth hormone poly A encoding region.

Surface expression of CD18 was analyzed by flow cytometry using the monoclonal antibody TS1/18. Heterodimer formation detected between α_d and CD18 in this cell line was consistent with the immunoprecipitation described in Example 10 with transient expression in COS cells.

Example 12

Human α_d binds to ICAM-R in a CD18-dependent fashion

In view of reports that demonstrate interactions between the leukocyte integrins and intercellular adhesion molecules (ICAMs) which mediate cell-cell contact [Hynes, *Cell 69*:11-25 (1992)], the ability of CHO cells expressing α_d/CD18 to bind ICAM-1, ICAM-R, or VCAM-1 was assessed by two methods.

In replicate assays, soluble ICAM-1, ICAM-R, or VCAM-1 IgG1 fusion proteins were immobilized on plastic and the ability of α_d/CD18 CHO transfected cells to bind the immobilized ligand was determined. Transfected cells were labeled internally with calcein, washed in binding buffer (RPMI with 1% BSA), and incubated in either buffer only (with or without 10 ng/ml PMA) or buffer with anti-CD18 monoclonal antibodies at 10 μg/ml. Transfected cells were added to 96-well Immulon 4 microtiter plates previously coated with soluble ICAM-1/IgG1, ICAM-R/IgG1 or VCAM-1/IgG1 fusion protein, or bovine serum albumin (BSA) as a negative control. Design of the soluble forms of these adhesion molecules is described and fully disclosed in co-pending and co-owned U.S. Patent Application Serial No. 08/102,852, filed August 5, 1993. Wells were blocked with 1% BSA in PBS prior to addition of labeled cells. After washing the plates by immersion in PBS with 0.1% BSA for 20 minutes, total fluorescence remaining in each well was measured using a Cytofluor 2300 (Millipore, Milford, MA).

In experiments with immobilized ICAMs, α_d/CD18 co-transfectants consistently showed a 3-5 fold increase in binding to ICAM-R/IgG1 wells over BSA coated wells. The specificity and CD18-dependence of this binding was demonstrated by the inhibitory effects of anti-CD18 antibody TS1/18. The binding of cells transfected with CD11a/CD18 to ICAM-1/IgG1 wells was comparable to the binding observed with BSA coated wells. CD11a/CD18 transfected cells showed a 2-3 fold increase in binding to ICAM-1/IgG1 wells only following pretreatment with PMA. PMA treatment of α_d/CD18 transfectants did not affect binding to ICAM-1/IgG1 or ICAM-R/IgG1 wells. No detectable binding of α_d/CD18 transfectants to VCAM-1/IgG1 wells was observed.

Binding of α_d/CD18-transfected cells to soluble ICAM-1/IgG1, ICAM-R/IgG1, or VCAM-1/IgG1 fusion proteins was determined by flow cytometry. Approximately one million α_d/CD18-transfected CHO cells (grown in spinner flasks for higher expression) per measurement were suspended in 100 μl

binding buffer (RPMI and 1% BSA) with or without 10 μg/ml anti-CD18 antibody. After a 20 minute incubation at room temperature, the cells were washed in binding buffer and soluble ICAM-1/IgG1 or ICAM-R/IgG1 fusion protein was added to a final concentration of 5 μg/ml. Binding was allowed to proceed for 30 minute at 37°C, after which the cells were washed three times and resuspended in 100 μl binding buffer containing FITC-conjugated sheep anti-human IgG1 at a 1:100 dilution. After a 30 minute incubation, samples were washed three times and suspended in 200 μl binding buffer for analysis with a Becton Dickinson FACScan.

Approximately 40-50% of the α_d/CD18 transfectants indicated binding to ICAM-R/IgG1, but no binding to ICAM-1/IgG1 or VCAM-1/IgG1 proteins. Pretreatment of transfected cells with PMA has no effect on α_d/CD18 binding to either ICAM-1/IgG1, ICAM-R/IgG1 or VCAM-1/IgG1, which was consistent with the immobilized adhesion assay. Binding by ICAM-R was reduced to background levels after treatment of α_d/CD18 transfectants with anti-CD18 antibody TS1/18.

The collective data from these two binding assays illustrate that α_d/CD18 binds to ICAM-R and does so preferentially as compared to ICAM-1 and VCAM-1. The α_d/CD18 binding preference for ICAM-R over ICAM-1 is opposite that observed with CD11a/CD18 and CD11b/CD18. Thus modulation of α_d/CD18 binding may be expected to selectively affect normal and pathologic immune function where ICAM-R plays a prominent role. Moreover, results of similar assays, in which antibodies immunospecific for various extracellular domains of ICAM-R were tested for their ability to inhibit binding of ICAM-R to α_d/CD18 transfectants, indicated that α_d/CD18 and CD11a/CD18 interact with different domains of ICAM-R.

The failure of CD11a/CD18 to bind ICAM-1/IgG1 or ICAM-R/IgG1 in solution suggests that the affinity of binding between CD11a/CD18 and ICAM-1 or ICAM-R is too low to permit binding in solution. Detection of

α_d/CD18 binding to ICAM-R/IgG1, however, suggests an unusually high binding affinity.

α_d Binding to iC3b

Complement component C3 can be proteolytically cleaved to form the complex iC3b, which initiates the alternative pathway of complement activation and leads ultimately to cell-mediated destruction of a target. Both CD11b and CD11c have been implicated in iC3b binding and subsequent phagocytosis of iC3b-coated particles. A peptide fragment in the CD11b I domain has recently been identified as the site of iC3b interaction [Ueda, *et al.*, *Proc.Natl.Acad.Sci.(USA) 91*:10680-10684 (1994)]. The region of iC3b binding is highly conserved in CD11b, CD11c, and α_d, suggesting an α_d/iC3b binding interaction.

Binding of α_d to iC3b is performed using transfectants or cell lines naturally expressing α_d (for example, PMA-stimulated HL60 cells) and iC3b-coated sheep red blood cells (sRBC) in a rosette assay [Dana, *et al.*, *J.Clin.Invest. 73*:153-159 (1984)]. The abilities of α_d/CD18 CHO transfectants, VLA4-CHO transfectants (negative control) and PMA-stimulated HL60 cells (positive control) to form rosettes are compared in the presence and absence of an anti-CD18 monoclonal antibody (for example TS1/18.1).

Example 13

Screening by Scintillation Proximity Assay

Specific inhibitors of binding between the α_d ligands of the present invention and their binding partners (α_d ligand/anti-ligand pair) may be determined by a variety of means, such as scintillation proximity assay techniques as generally described in U.S. Patent No. 4,271,139, Hart and Greenwald, *Mol.Immunol. 12*:265-267 (1979), and Hart and Greenwald, *J.Nuc.Med. 20*:1062-1065 (1979), each of which is incorporated herein by reference.

Briefly, one member of the α_d ligand/anti-ligand pair is bound to a solid support. A fluorescent agent is also bound to the support. Alternatively, the fluorescent agent may be integrated into the solid support as described in U.S. Patent No. 4,568,649, incorporated herein by reference. The non-support bound member of the α_d ligand/anti-ligand pair is labeled with a radioactive compound that emits radiation capable of exciting the fluorescent agent. When the ligand binds the radiolabeled anti-ligand, the label is brought sufficiently close to the support-bound fluorescer to excite the fluorescer and cause emission of light. When not bound, the label is generally too distant from the solid support to excite the fluorescent agent, and light emissions are low. The emitted light is measured and correlated with binding between the ligand and the anti-ligand. Addition of a binding inhibitor to the sample will decrease the fluorescent emission by keeping the radioactive label from being captured in the proximity of the solid support. Therefore, binding inhibitors may be identified by their effect on fluorescent emissions from the samples. Potential anti-ligands to α_d may also be identified by similar means.

Example 14

Soluble Human α_d Expression Constructs

The expression of full-length, soluble human α_d/CD18 heterodimeric protein provides easily purified material for immunization and binding assays. The advantage of generating soluble protein is that it can be purified from supernatants rather than from cell lysates (as with full-length membrane-bound α_d/CD18); recovery in therefore improved and impurities reduced.

The soluble α_d expression plasmid was constructed as follows. A nucleotide fragment corresponding to the region from bases 0 to 3161 in SEQ ID NO: 1, cloned into plasmid pATM.D12, was isolated by digestion with *Hind*III and *Aat*II. A PCR fragment corresponding to bases 3130 to 3390 in SEQ ID NO:

1, overlapping the *Hind*III/*Aat*II fragment and containing an addition *Mlu*I restriction site at the 3′ terminus, was amplified from pATM.D12 with primers sHAD.5 and sHAD.3 set out in SEQ ID NOS: 30 and 31, respectively.

5′-TTGCTGACTGCCTGCAGTTC-3′ (SEQ ID NO: 30)

5′-GTTCTGACGCGTAATGGCATTGTAGACCTCGTCTTC (SEQ ID NO: 31)

The PCR amplification product was digested with *Aat*II and *Mlu*I and ligated to the *Hind*III/*Aat*II fragment. The resulting product was ligated into *Hind*III/*Mlu*I-digested plasmid pDC1.s.

This construct is co-expressed with soluble CD18 in stably transfected CHO cells, and expression is detected by autoradiographic visualization of immunoprecipitated CD18 complexes derived from ^{35}S-methionine labeled cells. The construct is also co-expressed with CD18 in 293 cells [Berman, *et al., J.Cell.Biochem. 52*:183-195 (1993)].

Soluble Human α_d I Domain Expression Constructs

It has previously been reported that the I domain in CD11a can be expressed as an independent structural unit that maintains ligand binding capabilities and antibody recognition [Randi and Hogg, *J.Biol.Chem. 269*:12395-12398 (1994); Zhout, *et al., J.Biol.Chem. 269*:17075-17079 (1994); Michishita, *et al., Cell 72*:857-867 (1993)]. To generate a soluble fusion protein comprising the α_d I domain and human IgG4, the α_d I domain is amplified by PCR using primers designed to add flanking *Bam*HI and *Xho*I restriction sites to facilitate subcloning. These primers are set out in SEQ ID NOS: 32 and 33 with restriction sites underlined.

5′-ACGTATGCAGGATCCCATCAAGAGATGGACATCGCT (SEQ ID NO: 32)

5′-ACTGCATGTCTCGAGGCTGAAGCCTTCTTGGGACAT (SEQ ID NO: 33)

The C nucleotide immediately 3′ to the *Bam*HI site in SEQ ID NO: 32 corresponds to nucleotide 435 in SEQ ID NO: 1; the G nucleotide 3′ to the *Xho*I site in SEQ ID NO: 33 is complementary to nucleotide 1067 in SEQ ID NO: 1. The amplified I domain is digested with the appropriate enzymes, the purified fragment ligated into the mammalian expression vector pDCs and the prokaryotic expression vector pGEX-4T-3 (Pharmacia) and the I domain fragment sequenced. The fusion protein is then expressed in COS, CHO or *E.coli* cells transfected or transformed with an appropriate expression construct.

Given the affinity of α_d for ICAM-R, expression of the α_d I domain may be of sufficient affinity to be a useful inhibitor of cell adhesion in which α_d participates.

Analysis of Human α_d I Domain/IgG4 Fusion Proteins

Protein was resolved by SDS-PAGE under reducing and non-reducing conditions and visualized by either silver staining or Coomassie staining. Protein was then transferred to Immobilon PVDF membranes and subjected to Western blot analysis using anti-human IgG monoclonal antibodies or anti-bovine Ig monoclonal antibodies.

Protein detected was determined to migrate at about 120 kD under non-reducing conditions and at about 45 kD under reducing conditions. Minor bands were also detected on non-reducing gels at approximately 40-50 kD which were reactive with the anti-human, but not anti-bovine, antibodies. A 200 kD minor band was determined to be bovine Ig by Western blot.

Binding Assays Using I Domain Expression Products

The ability of the I domain to specifically recognize ICAM-R/IgG chimeric protein was tested in an ELISA format. Serial dilutions of α_d I domain IgG4 fusion protein ($I\alpha_d$/IgG4) in TBS were incubated with ICAM-1/IgG, ICAM-R/IgG, VCAM-1/IgG, or an irrelevant IgG1 myeloma protein

immobilized on Immulon IV RIA/EIA plates. CD11a I domain/IgG chimeric protein and human IgG4/kappa myeloma protein were used as negative controls. Bound IgG4 was detected with the biotinylated anti-IgG4 monoclonal antibody HP6023 followed by addition of strepavidin-peroxidase conjugate and development with substrate *o*-phenyldiamine.

In repeated assays, no binding of the CD11a/IgG4 protein or the IgG4 myeloma protein was detected with any of the immobilized proteins. The Iα_d/IgG4 protein did not bind to fish skin gelatin or bovine serum albumin blocking agents, human IgG1, or ICAM-1/IgG. A two to three fold increase in binding signal over background was detected in ICAM-R/IgG protein coated wells using 1-5 μg/ml concentrations of Iα_d/IgG4 protein. The signal in VCAM-1/IgG protein coated wells was 7-10 fold higher than background. In previous assays, α_d/CD18 transfected CHO cells did not bind VCAM-1/IgG protein, suggesting that VCAM-1 binding may be characteristic of isolated I domain amino acid sequences.

Additional α_d I domain constructs

Additional α_d I domain constructs are generated in the same fashion as the previous construct, but incorporating more amino acids around the α_d I domain. Specific constructs include: i) sequences from exon 5 (amino acids 127-353 in SEQ ID NO: 2), preceding the current construct, ii) the EF-hand repeats (amino acids 17-603 in SEQ ID NO: 2) following the I domain, and iii) the alpha chain truncated at the transmembrane region (amino acids 17-1029 in SEQ ID NO: 2), with an IgG4 tail for purification and detection purposes. These constructs are ligated into either the mammalian expression vector pDCS1 or the prokaryotic expression vector pGEX-4T-3 (Pharmacia) and the I domain sequenced. The fusion proteins are then be expressed in COS, CHO, or *E.coli* cells transformed or transfected with an appropriate expression construct. Protein are purified on a ProSepA column (Bioprocessing Limited, Durham, England),

tested for reactivity with the anti-IgG4 monoclonal antibody HP6023 and visualized on polyacrylamide gels with Coomassie staining.

In order to construct an expression plasmid for the entire α_d polypeptide, pATM.D12, described *supra*, is modified to express an α_d-IgG4 fusion protein by the following method. IgG4 encoding DNA is isolated from the vector pDCS1 by PCR using primers which individually incorporate a 5′ *Aat*II restriction site (SEQ ID NO: 89) and a 3′ *Xba*I restriction site (SEQ ID NO: 90).

5′-CGCTGTGACGTCAGAGTTGAGTCCAAATATGG-3′ (SEQ ID NO: 89)
5′-GGTGACACTATAGAATAGGGC-3′ (SEQ ID NO: 90)

Plasmid pATM.D12 is digested with *Aat*II and *Xba*I, and the appropriately digested and purified IgG4 PCR product ligated into the linear vector.

Example 15

Production of Human α_d-Specific Monoclonal Antibodies

Transiently transfected cells from Example 7 were washed three times in Dulbecco's phosphate buffered saline (D-PBS) and injected at 5 x 10^6 cells/mouse into Balb/c mice with 50 μg/mouse muramyl dipeptidase (Sigma) in PBS. Mice were injected two more times in the same fashion at two week intervals. The pre-bleed and immunized serum from the mice were screened by FACS analysis as outlined in Example 9 and the spleen from the mouse with the highest reactivity to cells transfected with α_d/CD18 was fused. Hybridoma culture supernatants were then screened separately for lack of reactivity against COS cells transfected with CD11a/CD18 and for reactivity with cells co-transfected with an α_d expression plasmid and CD18.

This method resulted in no monoclonal antibodies.

As an alternative for production of monoclonal antibodies, soluble α_d I domain IgG4 fusion protein was affinity purified from supernatant of stably transfected CHO cells and used to immunize Balb/c mice as described above. Hybridomas were established and supernatants from these hybridomas were screened by ELISA for reactivity against α_d I domain fusion protein. Positive cultures were then analyzed for reactivity with full length α_d/CD18 complexes expressed on CHO transfectants.

Mouse 1908 received three initial immunizations of α_d/CD18 transfected CHO cells and two subsequent boosts with soluble α_d/CD18 heterodimer. Two final immunizations included 50 μg/mouse Iα_d/IgG4 fusion protein. The fusion produced 270 IgG-producing wells. Supernatant from 45 wells showed at least 7-fold higher binding to Iα_d/IgG4 fusion protein than to human IgG4 by ELISA. None of the supernatants reacted to α_d/CD18 transfected CHO cells as determined by FACS analysis.

To determine whether the supernatants were able to recognize integrin alpha subunit proteins in another context, fresh frozen splenic sections

were stained with supernatants from 24 of the 45 wells. Three supernatants were determined to be positive: one stained large cells in the red pulp, while two others stained scattered cells in the red pulp and also trabeculae.

These supernatants were further analyzed by their ability to immunoprecipitate biotinylated CD18 complexes from either α_d/CD18 transfected CHO cells or PMA-stimulated HL60 cells. Fusion wells with supernatants that recognized protein in detergent lysates (which should not be as conformationally constrained as protein expressed as heterodimers) were selected for further subcloning. Monoclonal antibodies which recognize protein in detergent may be more useful in immunoprecipitation of heterodimeric complexes from transfectants, tissues, and cell lines.

As another alternative, monoclonal antibodies are generated as follows. Affinity purified α_d/CD18 heterodimeric protein from detergent lysates of stably transfected CHO cells is used with 50 μg/ml muramyl dipeptidase to immunize Balb/c mice as described above. Mice receive three immunizations before serum reactivity against α_d/CD18 is determined by immunoprecipitation of biotinylated complexes in the CHO transfectants. Hybridomas from positive animals are established according to standard protocols, after which hybridoma cultures are selected by flow cytometry using α_d/CD18 transfectants. CD11a/CD18 transfectants are utilized to control for CD18-only reactivity.

As another alternative for monoclonal antibody production, Balb/c mice undergo an immunization/immunosuppression protocol designed to reduce reactivity to CHO cell determinants on transfectants used for immunization. This protocol involves immunization with untransfected CHO cells and subsequent killing of CHO-reactive B-cell blasts with cyclophosphamide treatment. After three rounds of immunization and cyclophosphamide treatment are performed, the mice are immunized with α_d/CD18 CHO transfected cells as described above.

As still another alternative, heterodimeric CD18 complexes are immunoprecipitated from detergent lysates of whole spleen using an anti-CD18

monoclonal antibody, following preclearance of CD11a/CD18 and CD11b/CD18. CD11a/CD18 and CD11b/CD18 complexes are precleared by affinity chromatography using monoclonal antibodies TS2/4 and Mo1, respectively, coupled to a chromatographic resin. The remaining CD18 complexes are used as an immunogen in Balb/c mice for the first immunization. Three immunizations are given at three week intervals, the initial immunization administered in conjunction with Freund's Complete Adjuvant and the subsequent immunizations with Freund's Incomplete Adjuvant. Serum is assayed for α_d-specific reactivity by immunoprecipitation. Resulting hybridomas are screened by flow cytometry with α_d/CD18 CHO transfectants.

As another alternative, CD18 complexes from detergent lysates of PMA stimulated HL60 cells are enriched by preclearance as described above. Other β2 integrins are cleared on the same columns. Immunization with the resulting complexes, hybridoma production, and screening protocols are performed as described *supra*.

Example 16

Analysis of α_d distribution with polyclonal serum

Tissue distribution of α_d/CD18 was determined using polyclonal antiserum. Antiserum used to stain tissue was obtained from a mouse immunized 3 times with α_d transfected CHO cells (D6.CHO, α_d/CD18) with adjuvant peptide and once with purified α_d/CD18 heterodimer. A final boost included only α_d/CD18 heterodimer. Approximately 100 μl immunized serum was precleared by addition of approximately 10^8 LFA-1-transfected CHO cells for 2 hours at 4°C. The resulting serum was assayed for α_d reactivity at dilutions of 1/5000, 1/10000, 1/20000 and 1/40000 on normal human spleen. The polyclonal antibody was reactive at a dilution of 1/20000, while a 1/40000 dilution stained very weakly.

Once serum was determined to have specific α_d reactivity, it was used to stain various lymphoid and non-lymphoid tissues. Monoclonal antibodies recognizing CD18, CD11a, CD11b, and CD11c were used in the same experiment as controls. Staining of normal spleen sections with α_d polyclonal sera, and monoclonal antibodies to CD11a, CD11b, CD11c, and CD18 revealed the following results. The pattern observed with α_d polyclonal sera did not display the same pattern of labeling as CD11a, CD11b, CD11c, or CD18. There is a distinct pattern of labeling with some cells located in the marginal zone of the white pulp and a distinct labeling of cells peripheral to the marginal zone. This pattern was not observed with the other antibodies. Individual cells scattered throughout the red pulp were also labeled which may or may not be the same population or subset seen with CD11a and CD18.

Labeling with CD11c did display some cells staining in the marginal zone, but the antibody did not show the distinct ring pattern around the white pulp when compared to α_d polyclonal sera, nor did labeling in the red pulp give the same pattern of staining as α_d polyclonal sera.

Therefore, the labeling pattern seen with α_d polyclonal serum was unique compared to that seen using antibodies to the other β_2 integrins (CD11a, CD11b, CD11c, and CD18), and suggests that the *in vivo* distribution of α_d in man is dinstinct from that of other β_2 integrins.

Example 17

Isolation of Rat cDNA Clones

In view of the existence of both canine and human α_d subunits, attempts were made to isolate homologous genes in other species, including rat (this example) and mouse (Example 17, *infra*).

A partial sequence of a rat cDNA showing homology to the human α_d gene was obtained from a rat splenic λgt10 library (Clontech). The library was plated at 2 x 10^4 pfu/plate onto 150 mm LBM/agar plates. The library was

lifted onto Hybond membranes (Amersham), denatured 3 minutes, neutralized 3 minutes and washed 5 minutes with buffers as described in standard protocols [Sambrook, *et al.*, Molecular Cloning: a laboratory manual, p.2.110]. The membranes were placed immediately into a Stratalinker (Stratagene) and the DNA crosslinked using the autocrosslinking setting. The membranes were prehybridized and hybridized in 30% or 50% formamide, for low and high stringency conditions, respectively. Membranes were initially screened with a ^{32}P-labeled probe generated from the human α_d cDNA, corresponding to bases 500 to 2100 in clone 19A2 (SEQ ID NO: 1). The probe was labeled using Boehringer Mannheim's Random Prime Kit according to manufacturer's suggested protocol. Filters were washed with 2X SSC at 55°C.

Two clones, designated 684.3 and 705.1, were identified which showed sequence homology to human α_d, human CD11b, and human CD11c. Both clones aligned to the human α_d gene in the 3´ region of the gene, starting at base 1871 and extending to base 3012 for clone 684.3, and bases 1551 to 3367 for clone 705.1.

In order to isolate a more complete rat sequence which included the 5´ region, the same library was rescreened using the same protocol as employed for the initial screening, but using a mouse probe generated from clone A1160 (See Example 17, *infra*). Single, isolated plaques were selected from the second screening and maintained as single clones on LBM/agar plates. Sequencing primers 434FL and 434FR (SEQ ID NOS: 34 and 35, respectively) were used in a standard PCR protocol to generate DNA for sequencing.

5´-TATAGACTGCTGGGTAGTCCCCAC-3´ (SEQ ID NO: 34)

5´-TGAAGATTGGGGGTAAATAACAGA-3´ (SEQ ID NO: 35)

DNA from the PCR was purified using a Quick Spin Column (Qiagen) according to manufacturer's suggested protocol.

Two clones, designated 741.4 and 741.11, were identified which overlapped clones 684.3 and 705.1; in the overlapping regions, clones 741.1 and 741.11 were 100% homologous to clones 684.3 and 705.1. A composite rat cDNA having homology to the human α_d gene is set out in SEQ ID NO: 36; the predicted amino acid sequence is set forth in SEQ ID NO: 37.

Cloning of the 5´ end of Rat α_d

A 5´ cDNA fragment for the rat α_d gene was obtained using a Clonetech rat spleen RACE cloning kit according to manufacturer's suggested protocol. The gene specific oligonucleotides used were designated 741.11#2R and 741.2#1R (SEQ ID NOS: 59 and 58, respectively).

5´-CCAAAGCTGGCTGCATCCTCTC-3´ (SEQ ID NO: 59)
5´-GGCCTTGCAGCTGGACAATG-3´ (SEQ ID NO: 58)

Oligo 741.11#2R encompasses base pairs 131-152 in SEQ ID NO: 36, in the reverse orientation and 741.2#1R encompasses bases pairs 696-715 in SEQ ID NO: 36, also in the reverse orientation. A primary PCR was carried out using the 3´-most oligo, 741.2#1R. A second PCR followed using oligo 741.11#2R and DNA generated from the primary reaction. A band of approximately 300 base pairs was detected on a 1% agarose gel.

The secondary PCR product was ligated into plasmid pCRTAII (Invitrogen) according to manufacturer's suggested protocol. White (positive) colonies were picked and added to 100 μl LBM containing 1 μl of a 50 mg/ml carbenicillin stock solution and 1 μl M13 K07 phage culture in individual wells in a round bottom 96 well tissue culture plate. The mixture was incubated at 37°C for 30 minutes to one hour. Following the initial incubation period, 100 μl of LBM (containing 1 μl of 50 mg/ml carbenicillin and a 1:250 dilution of a 10

mg/ml kanamycin stock solution) were added and the incubation was continued overnight at 37°C.

Using a sterile 96 well metal transfer prong, supernatant from the 96 well plate was transferred to four Amersham Hybond nylon filters. The filters were denatured, neutralized and cross linked by standard protocols. The filters were prehybridized in 20 mls of prehybridization buffer (5X SSPE; 5X Denhardts; 1% SDS; 50 ugs/ml denatured salmon sperm DNA) at 50°C for several hours while shaking.

Oligo probes 741.11#1 and 741.11#1R (SEQ ID NOS: 56 and 57, respectively), encompassing base pairs 86-105 (SEQ ID NO: 36) in the forward and reverse orientation respectively, were labeled as follows.

5´-CCTGTCATGGGTCTAACCTG-3´ (SEQ ID NO: 56)
5´-AGGTTAGACCCATGACAGG-3´ (SEQ ID NO: 57)

Approximately 65 ng oligo DNA in 12 μl dH_20 was heated to 65°C for two minutes. Three μl of 10 mCi/ml γ-^{32}P-ATP were added to the tube along with 4 μl 5x Kinase Buffer (Gibco) and 1 μl T4 DNA Kinase (Gibco). The mixture was incubated at 37°C for 30 minutes. Following incubation, 16 μl of each labeled oligo probe were added to the prehybridization buffer and filters and hybridization was continued overnight at 42°C. The filters were washed three times in 5X SSPE; 0.1% SDS for 5 minutes per wash at room temperature, and autoradiographed for 6 hours. Positive clones were expanded and DNA purified using the Magic Mini Prep Kit (Promega) according to manufacturer's suggested protocol. Clone 2F7 was selected for sequencing and showed 100% homology to clone 741.11 in the overlapping region. The complete rat α_d nucleic acid sequence is set out in SEQ ID NO: 54; the amino acid sequence is set out in SEQ ID NO: 55.

Characteristics of the Rat cDNA and Amino Acid Sequences

Neither nucleic acid nor amino acid sequences have previously been reported for rat α subunits in β_2 integrins. However sequence comparisons to reported human β_2 integrin α subunits suggests that the isolated rat clone and its predicted amino acid sequence are most closely related to α_d nucleotide and amino acid sequences.

At the nucleic acid level, the isolated rat cDNA clone shows 80% identity in comparison to the human α_d cDNA; 68% identity in comparison to human CD11b; 70% identity in comparison to human CD11c; and 65% identity in comparison to mouse CD11b. No significant identity is found in comparison to human CD11a and to mouse CD11a.

At the amino acid level, the predicted rat polypeptide encoded by the isolated cDNA shows 70% identity in comparison to human α_d polypeptide; 28% identity in comparison to human CD11a; 58% identity in comparison to human CD11b; 61% identity in comparison to human CD11c; 28% identity in comparison to mouse CD11a; and 55% identity in comparison to mouse CD11b.

Example 18

Monoclonal Antibodies against Rat α_d I domain/Hu IgG4 Fusion Proteins

In view of the fact that the I domain of human β_2 integrins has been demonstrated to participate in ligand binding, it was assumed that the same would be true for rat α_d protein. Monoclonal antibodies immunospecific for the rat α_d I domain may therefore be useful in rat models of human disease states wherein α_d binding is implicated.

Oligos "rat alpha-DI5" (SEQ ID NO: 87) and "rat alpha-DI3" (SEQ ID NO: 88) were generated from the rat α_d sequence corresponding to base pairs 469-493 and base pairs 1101-1125 (in the reverse orientation), respectively, in SEQ ID NO: 54. The oligos were used in a standard PCR reaction to generate a rat α_d DNA fragment containing the I domain spanning base pairs 459-1125 in

SEQ ID NO: 54. The PCR product was ligated into vector pCRTAII (Invitrogen) according to manufacturer's suggested protocol. A positive colony was selected and expanded for DNA purification using a Qiagen (Chatswoth, GA) Midi Prep kit according to manufacturer's protocol. The DNA was digested with *Xho*I and *Bgl*II in a standard restriction enzyme digest and a 600 base pair band was gel purified which was subsequently ligated into pDCS1/HuIgG4 expression vector. A positive colony was selected, expanded and DNA purified with a Quiagen Maxi Prep Kit.

COS cells were plated at half confluence on 100mm culture dishes and grown overnight at 37°C in 7% CO_2. Cells were rinsed once with 5 ml DMEM. To 5 ml DMEM, 50 μl DEAE-Dextran, 2 μl chloroquine and 15 μg rat α_d I domain/HulgG4 DNA described above was added. The mixture was added to the COS cells and incubated at 37°C for 3 hours. Media was then removed and 5 ml 10% DMSO in CMF-PBS was added for exactly one minute. The cells were gently rinsed once with DMEM. Ten ml DMEM containing 10% FBS was added to the cells and incubation continued overnight at 37°C in 7% CO_2. The next day, media was replaced with fresh media and incubation continued for three additional days. The media was harvested and fresh media was added to the plate. After three days, the media was collected again and the plates discarded. The procedure was repeated until 2 liters of culture supernatant were collected.

Supernatant collected as described above was loaded onto a Prosep-A column (Bioprocessing Limited) and protein purified as described below.

The column was initially washed with 15 column volumes of Wash Buffer containing 35 mM Tris and 150 mM NaCl, pH 7.5. Supernatant was loaded at a slow rate of less than approximately 60 column volumes per hour. After loading, the column was washed with 15 column volumes of Wash Buffer, 15 column volumes of 0.55 M diethanolamine, pH 8.5, and 15 column volumes

50 mM citric acid, pH 5.0. Protein was eluted with 50 mM citric acid, pH 3.0. Protein was neutralized with 1.0 M Tris, pH 8.0, and dialyzed in sterile PBS.

The rat α_d I domain protein was analyzed as described in Example 14. The detected protein migrated in the same manner as observed with human I domain protein.

Immunization Protocol

Mice were individually immunized with 50 μg purified rat α_d I domain/HulgG4 fusion protein previously emulsified in an equal volume of Freunds Complete Adjuvant (FCA) (Sigma). Approximately 200 μl of the antigen/adjuvant preparation was injected at 4 sites in the back and flanks of each of the mice. Two weeks later the mice were boosted with an injection of 100 μl rat α_d I domain/HuIgG4 antigen (50 μg/mouse) previously emulsified in an equal volume of Freunds Incomplete Adjuvant (FIA). After two additional weeks, the mice were boosted with 50 μg antigen in 200 μl PBS injected intravenously.

To evaluate serum titers in the immunized mice, retro-orbital bleeds were performed on the animals ten days following the third immunization. The blood was allowed to clot and serum isolated by centrifugation. The serum was used in an immunoprecipitation on biotinylated (BIP) rat splenocytes. Serum from each mouse immunoprecipitated protein bands of expected molecular weight for rat α_d and rat CD18. One mouse was selected for the fusion and was boosted a fourth time as described above for the third boost.

The hybridoma supernatants were screened by antibody capture, described as follows. Immulon 4 plates (Dynatech, Cambridge, Massachusetts) were coated at 4°C with 50 μl/well goat anti-mouse IgA, IgG or IgM (Organon Teknika) diluted 1:5000 in 50 mM carbonate buffer, pH 9.6. Plates were washed 3X with PBS containing 0.05% Tween 20 (PBST) and 50 μl culture supernatant was added. After incubation at 37°C for 30 minutes, and washing as described above, 50 μl horseradish peroxidase-conjugated goat anti-mouse IgG9(Fc)

(Jackson ImmunoResearch, West Grove, Pennsylvania) diluted 1:3500 in PBST was added. Plates were incubated as described above and washed 4X with PBST. Immediately thereafter, 100μl substrate, containing 1 mg/ml *o*-phenylene diamine (Sigma) and 0.1 μl/ml 30% H_2O_2 in 100 mM citrate, pH4.5, was added. The color reaction was stopped after 5 minutes with the addition of 50 μl 15% H_2SO_4. Absorbance at 490 nm was read on a Dynatech plate reader.

Supernatant from antibody-containing wells was also analyzed by ELISA with immobilized rat α_d I domain/HulgG4 fusion protein. An ELISA with HuIgG4 antibody coated plates served as a control for reactivity against the IgG fusion partner. Positive wells were selected for further screening by BIP on rat splenocyte lysates using techniques described below.

Biotinylation of Cell Surface Antigens

Rats were sacrificed by asphyxiation with CO_2 and spleens were removed using standard surgical techniques. Splenocytes were harvested by gently pushing the spleen through a wire mesh with a 3 cc syringe plunger in 20 mls RPMI. Cells were collected into a 50 ml conical tube and washed in the appropriate buffer.

Cells were washed three times in cold D-PBS and resuspended at a density of 10^8 to 10^9 cells in 40 ml PBS. Four mg of NHS-Biotin (Pierce) was added to the cell suspension and the reaction was allowed to continue for exactly 15 minutes at room temperature. The cells were pelleted and washed three times in cold D-PBS.

Cell Lysates

Cells were resuspended at a density of 10^8 cells/ml in cold lysis Buffer (1% NP40; 50 mM Tris-HCl, pH 8.0; 150 mM NaCl; 2 mM CaCl; 2 mM MgCl; 1:100 solution of pepstain, leupeptine, and aprotinin, added just before adding to cells; and 0.0001 g PMSF crystals, added just before adding to cells).

Lysates were vortexed for approximately 30 seconds, incubated for 5 minute at room temperature, and further incubated for 15 minutes on ice. Lysates were centrifuged for 10 minutes at 10,000 xg to pellet the insoluble material. Supernatant was collected into a new tube and stored at between 4°C and -20°C.

Immunoprecipitation

One ml cell lysate was precleared by incubation with 200 μl of a protein A sepharose slurry (Zymed) overnight at 4°C. Precleared lysate was aliquoted into Eppendorf tubes at 50 μl/tube for each antibody to be tested. Twenty-five μl of polyclonal serum or 100 to 500 μl of monoclonal antibody supernatant were added to the precleared lysates and the resulting mixture incubated for 2 hours at 4°C with rotation. One hundred μl rabbit anti-mouse IgG (Jackson) bound to protein A sepharose beads in a PBS slurry was then added and incubation continued for 30 minutes at room temperature with rotation. Beads were pelleted with gentle centrifugation, and washed three times with cold Wash Buffer (10 mM HEPES; 0.2 M NaCl; 1% Trition X-100). Supernatant was removed by aspiration, and 20 μl 2X SDS sample buffer containing 10% β-mercaptoethanol was added. The sample was boiled for 2 minutes in a water bath, and the sample loaded onto a 5% SDS PAGE gel. Following separation, the proteins were transferred to nitrocellulose at constant current overnight. The nitrocellulose filters were blocked with 3% BSA in TBS-T for 1 hour at room temperature and the blocking buffer was removed. A 1:6000 dilution of Strepavidin-HRP conjugate (Jackson) in 0.1% BSA TBS-T was added and incubation continued for 30 minutes at room temperature. Filters were washed three times for 15 minutes each with TBS-T and autoradiographed using Amersham's ECL kit according to manufacturer's suggested protocol.

Example 19

Isolation of Mouse cDNA Clones

Isolation of a mouse α_d homolog was attempted.

Cross-species hybridization was performed using two PCR-generated probes: a 1.5 kb fragment corresponding to bases 522 to 2047 from human clone 19A2 (SEQ ID NO: 1), and a 1.0 kb rat fragment which corresponds to bases 1900 to 2900 in human clone 19A2 (SEQ ID NO: 1). The human probe was generated by PCR using primer pairs designated ATM-2 and 9-10.1 set out in SEQ ID NOS: 38 and 39, respectively; the rat probe was generated using primer pairs 434L and 434R, set out in SEQ ID NOS: 34 and 35, respectively. Samples were incubated at 94°C for 4 minutes and subjected to 30 cycles of the temperature step sequence: 94°C; 50°C 2 minutes; 72°C, 4 minutes.

5′-GTCCAAGCTGTCATGGGCCAG-3′ (SEQ ID NO: 38)
5′-GTCCAGCAGACTGAAGAGCACGG-3′ (SEQ ID NO: 39)

The PCR products were purified using the Qiagen Quick Spin kit according to manufacturer's suggested protocol, and approximately 180 ng DNA was labeled with 200 μCi [^{32}P]-dCTP using a Boehringer Mannheim Random Primer Labeling kit according to manufacturer's suggested protocol. Unincorporated isotope was removed using a Centri-sep Spin Column (Princeton Separations, Adelphia, NJ) according to manufacturer's suggested protocol. The probes were denatured with 0.2 N NaOH and neutralized with 0.4 M Tris-HCl, pH 8.0, before use.

A mouse thymic oligo dT-primed cDNA library in lambda ZAP II (Stratagene) was plated at approximately 30,000 plaques per 15 cm plate. Plaque lifts on nitrocellulose filters (Schleicher & Schuell, Keene, NH) were incubated at 50°C with agitation for 1 hour in a prehybridization solution (8 ml/lift) containing 30% formamide. Labeled human and rat probes were added to the

prehybridization solution and incubation continued overnight at 50°C. Filters were washed twice in 2X SSC/0.1% at room temperature, once in 2X SSC/0.1% SDS at 37°C, and once in 2X SSC/0.1% SDS at 42°C. Filters were exposed on Kodak X-Omat AR film at -80°C for 27 hours with an intensifying screen.

Four plaques giving positive signals on duplicate lifts were restreaked on LB medium with magnesium (LBM)/carbenicillin (100 mg/ml) plates and incubated overnight at 37°C. The phage plaques were lifted with Hybond filters (Amersham), probed as in the initial screen, and exposed on Kodak X-Omat AR film for 24 hours at -80°C with an intensifying screen.

Twelve plaques giving positive signals were transferred into low Mg^{++} phage diluent containing 10 mM Tris-HCl and 1 mM $MgCl_2$. Insert size was determined by PCR amplification using T3 and T7 primers (SEQ ID NOS: 13 and 14, respectively) and the following reaction conditions. Samples were incubated at 94°C for 4 minutes and subjected to 30 cycles of the temperature step sequence: 94°C, for 15 seconds; 50°C, for 30 seconds; and 72°C for 1 minute.

Six samples produced distinct bands that ranged in size from 300 bases to 1 kb. Phagemids were released via co-infection with helper phage and recircularized to generate Bluescript SK^- (Stratagene). The resulting colonies were cultured in LBM/carbenicillin (100 mg/ml) overnight. DNA was isolated with a Promega Wizard miniprep kit (Madison, WI) according to manufacturer's suggested protocol. *Eco*RI restriction analysis of purified DNA confirmed the molecular weights which were detected using PCR. Insert DNA was sequenced with M13 and M13 reverse.1 primers set out in SEQ ID NOS: 40 and 41, respectively.

5′-TGTAAAACGACGGCCAGT-3′ (SEQ ID NO: 40)

5′-GGAAACAGCTATGACCATG-3′ (SEQ ID NO: 41)

Sequencing was performed as described in Example 4.

Of the six clones, only two, designated 10.3-1 and 10.5-2, provided sequence information and were identical 600 bp fragments. The 600 bp sequence was 68% identical to a corresponding region of human α_d, 40% identical to human CD11a, 58% identical to human CD11c, and 54% identical to mouse CD11b. This 600 bp fragment was then utilized to isolate a more complete cDNA encoding a putative mouse α_d homolog .

A mouse splenic cDNA library (oligo dT^- and random-primed) in lambda Zap II (Stratagene) was plated at 2.5 x 10^4 phage/15 cm LBM plate. Plaques were lifted on Hybond nylon transfer membranes (Amersham), denatured with 0.5 M NaOH/1.5 M NaCl, neutralized with 0.5 M Tris Base/1.5 M NaCl/11.6 HCl, and washed in 2X SSC. The DNA was cross-linked to filters by ultraviolet irradiation.

Approximately 500,000 plaques were screened using probes 10.3-1 and 10.5-2 previously labeled as described *supra*. Probes were added to a prehybridization solution and incubated overnight at 50°C. The filters were washed twice in 2X SSC/0.1% SDS at room temperature, once in 2X SSC/0.1% SDS at 37°C, and once in 2X SSC/0.1% SDS at 42°C. Filters were exposed on Kodak X-Omat AR film for 24 hours at -80°C with an intensifying screen. Fourteen plaques giving positive signals on duplicate lifts were subjected to a secondary screen identical to that for the initial screen except for additional final high stringency washes in 2X SSC/ 0.1% SDS at 50°C, in 0.5X SSC/0.1% SDS at 50°C, and at 55°C in 0.2X SSC/0.1% SDS. The filters were exposed on Kodak X-Omat AR film at -80°C for 13 hours with an intensifying screen.

Eighteen positive plaques were transferred into low Mg^{++} phage diluent and insert size determined by PCR amplification as described above. Seven of the samples gave single bands that ranged in size from 600 bp to 4 kb. *Eco*RI restriction analysis of purified DNA confirmed the sizes observed from

PCR and the DNA was sequenced with primers M13 and M13 reverse.1 (SEQ ID NOS: 40 and 41, respectively).

One clone designated B3800 contained a 4 kb insert which corresponded to a region 200 bases downstream of the 5′ end of the human α_d 19A2 clone and includes 553 bases of a 3′ untranslated region. Clone B3800 showed 77% identity to a corresponding region of human α_d, 44% identity to a corresponding region of human CD11a, 59% identity to a corresponding region of human CD11c, and 51% identity to a corresponding region of mouse CD11b. The second clone A1160 was a 1.2 kb insert which aligned to the 5′ end of the coding region of human α_d approximately 12 nucleic acids downstream of the initiating methionine. Clone A1160 showed 75% identity to a corresponding region of human α_d, 46% identity to a corresponding region of human CD11a, 62% identity to a corresponding region of human CD11c, and 66% identity to a corresponding region of mouse CD11b.

Clone A1160, the fragment closer to the 5′ end of human clone 19A2, is 1160 bases in length, and shares a region of overlap with clone B3800 starting at base 205 and continuing to base 1134. Clone A1160 has a 110-base insertion (bases 704-814 of clone A1160) not present in the overlapping region of clone B3800. This insertion occurs at a probable exon-intron boundary [Fleming, *et al., J.Immunol. 150*:480-490 (1993)] and was removed before subsequent ligation of clones A1160 and B3800.

Rapid Amplification of 5′ cDNA End of the Putative Mouse α_d Clone

RACE PCR [Frohman, "RACE: Rapid Amplification of cDNA Ends," in PCR Protocols: A Guide to Methods and Applications, Innis, *et al.* (eds.) pp. 28-38, Academic Press:New York (1990)] was used to obtain missing 5′ sequences of the putative mouse α_d clone, including 5′ untranslated sequence and initiating methionine. A mouse splenic RACE-Ready kit (Clontech, Palo Alto, CA) was used according to the manufacturer's suggested protocol. Two

antisense, gene-specific primers, A1160 RACE1-primary and A1160 RACE2-nested (SEQ ID NOS: 42 and 43), were designed to perform primary and nested PCR.

5′-GGACATGTTCACTGCCTCTAGG-3′ (SEQ ID NO: 42)

5′-GGCGGACAGTCAGACGACTGTCCTG-3′ (SEQ ID NO: 43)

The primers, SEQ ID NOS: 42 and 43, correspond to regions starting 302 and 247 bases from the 5′ end, respectively. PCR was performed as described, *supra*, using the 5′ anchor primer (SEQ ID NO: 44) and mouse spleen cDNA supplied with the kit.

5′-CTGGTTCGGCCCACCTCTGAAGGTTCCAGAATCGAT(SEQ ID NO: 44)

Electrophoresis of the PCR product revealed a band approximately 280 bases in size, which was subcloned using a TA cloning kit (Invitrogen) according to manufacturer's suggested protocol. Ten resulting colonies were cultured, and the DNA isolated and sequenced. An additional 60 bases of 5′ sequence were identified by this method, which correspond to bases 1 to 60 in SEQ ID NO: 45.

Characteristics of the Mouse cDNA and Predicted Amino Acid Sequence

A composite sequence of the mouse cDNA encoding a putative homolog of human α_d is set out in SEQ ID NO: 45. Although homology between the external domains of the human and mouse clones is high, homology between the cytoplasmic domains is only 30%. The observed variation may indicate C-terminal functional differences between the human and mouse proteins. Alternatively, the variation in the cytoplasmic domains may result from splice variation, or may indicate the existence of an additional β_2 integrin gene(s).

At the amino acid level, the mouse cDNA predicts a protein (SEQ ID NO: 46) with 28% identity to mouse CD11a, 53% identity to mouse CD11b, 28% identity to human CD11a, 55% identity to human CD11b, 59% identity to human CD11c, and 70% identity to human α_d. Comparison of the amino acid sequences of the cytoplasmic domains of human α_d and the putative mouse homolog indicates regions of the same length, but having divergent primary structure. Similar sequence length in these regions suggests species variation rather than splice variant forms. When compared to the predicted rat polypeptide, Example 16, *supra*, mouse and rat cytoplasmic domains show greater than 60% identity.

Example 20

Isolation of additional mouse αd cDNA clones for sequence verification

In order to verify the nucleic and amino acids sequences describe in Example 19 for mouse α_d, additional mouse sequences were isolated for the purposes of confirmation.

Isolation of mouse cDNA by hybridization with two homologous α_d probes (3´ and 5´) was performed using both a mouse splenic random primed library and an oligo dT-primed cDNA library in lambda ZAP II (Strategene). The library was plated at 5 x 10^5 phage per 15 cm LBM plate. Plaques were lifted on Hybond nylon membranes (Amersham), and the membranes were denatured (0.5 M NaOH/1.5 M NaCl), neutralized (0.5 M Tris Base/1.5 M NaCl / 11.6 M HCl) and washed (2X SSC salt solution). DNA was cross-lined to filters by ultraviolet irradiation.

Probes were generated using primers described below in a PCR reaction under the following conditions. Samples were held at 94°C for 4 minutes and then run through 30 cycles of the temperature step sequence (94°C for 15 seconds; 50°C for 30 seconds; 72°C for 1 minute in a Perkin-Elmer 9600 thermocycler).

The 3′ probe was approximately 900 bases long and spanned a region from nucleotides 2752 to 3651 (in SEQ ID NO: 1) (5′ → 3′) and was produced with primers 11.b-1/2FOR11 and 11.b-1/2REV2 as shown in SEQ ID NOS: 69 and 74, respectively. This probe was used in a first set of lifts.

The 5′ probe was approximately 800 bases long and spanned a region from nucleotides 149 to 946 (in SEQ ID NO: 1) (5′ → 3′) and was produced with primers 11.b-1/2FOR1 and 11.a-1/1REV1 as shown in SEQ ID NOS: 50 and 85, respectively). This probe was used in a second set of lifts.

In a third set of lifts, both probes described above were used together on the same plates.

Approximately 500,000 plaques were screened using the two probes from above which were labeled in the same way as described in Example 17. Labeled probes were added to a prehybridization solution, containing 45% formamide, and incubated overnight at 50°C. Filters were washed twice in 2X SSC/0.1% SDS at room temperature (22°C). A final wash was carried out in 2X SSC/0.1% SDS at 50°C. Autoradiography was for 19 hours at -80°C on Kodak X-Omat AR film with an intensifying screen.

Thirteen plaques giving positive signals on at least duplicate lifts were subjected to a secondary screen performed as described for the initial screen except that both the 3′ and 5′ labeled probes were used for hybridization and an additional final wash was incorporated using 2X SSC/0.1% SDS at 65′C. Autoradiography was performed as described above for 2.5 hours.

Thirteen plaques (designated MS2P1 through MS2P13) giving positive signals were transferred into low Mg^{++} phage diluent. Insert size was determined by PCR amplification (Perkin-Elmer 9600 thermocycler) using T3 and T7 primers which anneal to Bluescript phagemid in ZAP II (sequence previously described) under the same conditions shown above. Band sizes ranged from 500 bases to 4Kb. Phagemids were isolated, prepared, and sequenced with M13 and M13 reverse.1 primers (SEQ ID NOS: 40 and 41, respectively). Five of the

thirteen clones; MS2P-3, MS2P-6, MS2P-9, MS2P-12, and MS2P-13, were sequenced, and together, represented a region from approximately base 200 at the 5′ end to about 300 bases past a first stop codon at the 3′ end.

Automated sequencing was performed as described in Example 4 by first using M13 and M13 reverse.1 primers (SEQ ID NOS: 40 and 41, respectively) to sequence the ends of each clone and to determine its position relative to construct #17 (SEQ ID NO: 45). Each clone was then completely sequenced using the appropriate primers (listed below) for that particular region.

11.b-1/2FOR1	5′-GCAGCCAGCTTCGGACAGAC-3′	(SEQ ID NO: 50)
11.a-1/1FOR2	5′-CCGCCTGCCACTGGCGTGTGC-3′	(SEQ ID NO: 60)
11.a-1/1FOR3	5′-CCCAGATGAAGGACTTCGTCAA-3′	(SEQ ID NO: 61)
11.b-1/2FOR4	5′-GCTGGGATCATTCGCTATGC-3′	(SEQ ID NO: 62)
11.b-1/2FOR5	5′-CAATGGATGGACCAGTTCTGG-3′	(SEQ ID NO: 63)
11.b-1/2FOR6	5′-CAGATCGGCTCCTACTTTGG-3′	(SEQ ID NO: 64)
11.b-1/2FOR7	5′-CATGGAGCCTCGAGACAGG-3′	(SEQ ID NO: 65)
11.b-1/2FOR8	5′-CCACTGTCCTCGAAGCTGGAG-3′	(SEQ ID NO: 66)
11.b-1/2FOR9	5′-CTTCGTCCTGTGCTGGCTGTGGGCTC-3	(SEQ ID NO: 67)
11.b-1/2FOR10	5′-CGCCTGGCATGTGAGGCTGAG-3′	(SEQ ID NO: 68)
11.b-1/2FOR11	5′-CCGTGATCAGTAGGCAGGAAG-3′	(SEQ ID NO: 69)
11.b-1/2FOR12	5 -GTCACAGAGGGAACCTCC-3′	(SEQ ID NO: 70)
11.b-1/2FOR13	5′-GCTCCTGAGTGAGGCTGAAATCA-3′	(SEQ ID NO: 71)
11.b-1/2FOR14	5′-GAGATGCTGGATCTACCATCTGC-3′	(SEQ ID NO: 72)
11.b-1/2FOR15	5′-CTGAGCTGGGAGATTTTTATGG-3′	(SEQ ID NO: 73)
11.b-1/2REV2	5′-GTGGATCAGCACTGAAATCTG-3′	(SEQ ID NO: 74)
11.b-1/2REV3	5′-CGTTTGAAGAAGCCAAGCTTG-3′	(SEQ ID NO: 75)
11.b-1/2REV4	5′-CACAGCGGAGGTGCAGGCAG-3′	(SEQ ID NO: 76)
11.b-1/2REV5	5′-CTCACTGCTTGCGCTGGC-3′	(SEQ ID NO: 77)

11.b-1/2REV6	5′-CGGTAAGATAGCTCTGCTGG-3′	(SEQ ID NO: 78)
11.b-1/2REV7	5′-GAGCCCACAGCCAGCACAGG-3′	(SEQ ID NO: 79)
11.b-1/2REV8	5′-GATCCAACGCCAGATCATACC-3′	(SEQ ID NO: 80)
11.b-1/2REV9	5′-CACGGCCAGGTCCACCAGGC-3′	(SEQ ID NO: 81)
11.b-1/2REV10	5′-CACGTCCCCTAGCACTGTCAG-3′	(SEQ ID NO: 82)
11.b-1/2REV11	5′-CCATGTCCACAGAACAGAGAG-3′	(SEQ ID NO: 51)
11.b-1/2REV12	5′-TTGACGAAGTCCTTCATCTGGG-3′	(SEQ ID NO: 83)
11.b-1/2REV13	5′-GAACTGCAAGCTGGAGCCCAG-3′	(SEQ ID NO: 84)
11.a-1/1REV1	5′-CTGGATGCTGCGAAGTGCTAC-3′	(SEQ ID NO: 85)
11.a-1/1REV2	5′-GCCTTGGAGCTGGACGATGGC-3′	(SEQ ID NO: 86)

Sequences were edited, aligned, and compared to a previously isolated mouse α_d sequence (construct #17, SEQ ID NO: 45).

Alignment of the new sequences revealed an 18 base deletion in construct #17 beginning at nucleotide 2308; the deletion did not cause a shift in the reading frame. Clone MS2P-9, sequenced as described above, also revealed the same 18 base deletion. The deletion has been observed to occur in 50% of mouse clones that include the region but has not been detected in rat or human α_d clones. The eighteen base deletion is characterized by a 12 base palindromic sequence AAGCAGGAGCTCCTGTGT (SEQ ID NO: 91). This inverted repeat in the nucleic acid sequence is self-complementary and may form a loop out, causing cleavage during reverse transcription. The mouse α_d sequence which includes the additional 18 bases is set forth in SEQ ID NO: 52; the deduced amino acid sequence is set forth in SEQ ID NO: 53.

Example 21

In situ hybridizations in Mouse

Tissue distribution was then determined for mouse α_d in order to provide a comparison to that in humans, described in Example 6.

A single stranded 200 bp mRNA probe was generated from a DNA template, corresponding to nucleotides 3460 to 3707 in the cytoplasmic tail region of the murine cDNA, by *in vitro* RNA transcription incorporating ^{35}S-UTP (Amersham).

Whole mouse embryos (harvested at days 11-18 after fertilization) and various mouse tissues, including spleen, kidney, liver, intestine, and thymus, were hybridized *in situ* with the radiolabeled single-stranded mRNA probe.

Tissues were sectioned at 6 μm thickness, adhered to Vectabond (Vector Laboratories, Inc., Burlingame, CA) coated slides, and stored at -70°C. Prior to use, slides were removed from -70°C and placed at 50°C for approximately 5 minutes. Sections were fixed in 4% paraformaldehyde for 20 minutes at 4°C, dehydrated with an increasing ethanol gradient (70-95-100%) for 1 minute at 4°C at each concentration, and air dried for 30 minutes at room temperature. Sections were denatured for 2 minutes at 70°C in 70% formamide/2X SSC, rinsed twice in 2X SSC, dehydrated with the ethanol gradient described *supra* and air dried for 30 minutes. Hybridization was carried out overnight (12-16 hours) at 55°C in a solution containing ^{35}S-labeled riboprobes at 6 x 10^5 cpm/section and diethylpyrocarbonate (DEPC)-treated water to give a final concentration of 50% formamide, 0.3 M NaCl, 20 mM Tris-HCl, pH 7.5, 10% dextran sulfate, 1X Denhardt's solution, 100 mM dithiothreitol (DTT) and 5 mM EDTA. After hybridization, sections were washed for 1 hour at room temperature in 4X SSC/10 mM DTT, 40 minutes at 60°C in 50% formamide/2X SSC/10 mM DTT, 30 minutes at room temperature in 2X SSC, and 30 minutes at room temperature in 0.1X SSC. The sections were dehydrated, air dried for 2 hours, coated with Kodak NTB2 photographic emulsion, air dried for 2 hours,

developed (after storage at 4°C in complete darkness) and counterstained with hematoxylin/eosin.

Spleen tissue showed a strong signal primarily in the red pulp. This pattern is consistent with that of tissue macrophage distribution in the spleen, but does not exclude other cell types.

Example 22

Generation of Mouse Expression Constructs

In order to construct an expression plasmid including mouse cDNA sequences exhibiting homology to human α_d, inserts from clones A1160 and B3800 were ligated. Prior to this ligation, however, a 5′ leader sequence, including an initiating methionine, was added to clone A1160. A primer designated "5′ PCR leader" (SEQ ID NO: 47) was designed to contain: (1) identical nonspecific bases at positions 1-6 allowing for digestion; (2) a *Bam*HI site (underlined in SEQ ID NO: 47) from positions 7-12 to facilitate subcloning into an expression vector; (3) a consensus Kozak sequence from positions 13-18, (4) a signal sequence including a codon for an initiating methionine (bold in SEQ ID NO: 47), and (5) an additional 31 bases of specifically overlapping 5′ sequence from clone A1160 to allow primer annealing. A second primer designated "3′ end frag" (SEQ ID NO: 48) was used with primer "5′ PCR leader" to amplify the insert from clone A1160.

5′-AGTTACGGATCCGGCACC**ATG**AC-
-CTTCGGCACTGTGATCCTCCTGTGTG-3′ (SEQ ID NO: 47)

5′-GCTGGACGATGGCATCCAC-3′ (SEQ ID NO: 48)

The resulting PCR product did not digest with *Bam*HI, suggesting that an insufficient number of bases preceded the restriction site, prohibiting

recognition by the enzyme. The length of the "tail" sequence preceding the *Bam*HI site in the 5′ primer (SEQ ID NO: 47) was increased and PCR was repeated on the amplification product from the first PCR. A 5′ primer, designated mAD.5′.2 (SEQ ID NO: 49), was designed with additional nonspecific bases at positions 1-4 and an additional 20 bases specifically overlapping the previously employed "5′ PCR leader" primer sequences.

5′-GTAGAGTTACGGATCCGGCACCAT-3′ (SEQ ID NO: 49)

Primers "mAD.5′.2" and "3′ end frag" were used together in PCR with the product from the first amplification as template. A resulting secondary PCR product was subcloned into plasmid pCRtmII (Invitrogen) according to manufacturer's suggested protocol and transformed into competent One shot cells (Invitrogen). One clone containing the PCR product was identified by restriction enzyme analysis using *Bam*HI and *Eco*RI and sequenced. After the sequence was verified, the insert was isolated by digestion with *Bam*HI and *Eco*RI and gel purified.

The insert from clone B3800 was isolated by digestion with *Eco*RI and *Not*I, gel purified, and added to a ligation reaction which included the augmented A1160 *Bam*HI/*Eco*RI fragment. Ligation was allowed to proceed for 14 hours at 14°C. Vector pcDNA.3 (Invitrogen), digested with *Bam*HI and *Not*I, was added to the ligation reaction with additional ligase and the reaction was continued for another 12 hours. An aliquot of the reaction mixture was transformed into competent *E. coli* cells, the resulting colonies cultured, and one positive clone identified by PCR analysis with the primers 11.b-1/2FOR1 and 11.b-1/2REV11 (SEQ ID NOS: 50 and 51, respectively). These primers bridge the A1160 and B3800 fragments, therefore detection of an amplification product indicates the two fragments were ligated. The sequence of the positive clone was

thymidine kinase encoding cassettes. Further analysis of this clone with an I domain probe (corresponding to nucleotides 454-1064 in SEQ ID NO: 45) indicated that the clone did not contain I domain encoding sequences.

Using the same I domain probe, the λFIXII genomic library was rescreened. Initially, six positive clones were detected, one of which remained positive upon secondary screening. DNA isolated from this clone reacted strongly in Southern analysis with an I domain probe. No reactivity was detected using the original 750 bp probe, however, indicating that this clone included regions 5′ to nucleotides 1985-2773 of SEQ ID NO: 45..

Alternatively, the lack of hybridization to the 750 bp probe may have suggested that the clone was another member of the integrin family of proteins. To determine if this explanation was plausible, the 13 kb insert was subcloned into pBluescript SKII$^+$. Purified DNA was sequenced using primers corresponding to α_d I domain nucleic acid sequences 441-461, 591-612, 717-739, and reverse 898-918 in SEQ ID NO: 52. Sequence information was obtained using only the first 4441-4461 primer, and only the 5′-most exon of the I domain was efficiently amplified. The remainder of the I domain was not amplified. The resulting clone therefore comprised exon 6 of the mouse α_d gene, and intronic sequences to the 3′ and 5′ end of the exon. Exon 7 was not represented in the clone. After sequencing, a construct is generated containing neomycin resistance and thymidine kinase genes.

The neomycin resistance (neo^r) gene is inserted into the resulting plasmid in a manner that interrupts the protein coding sequence of the genomic mouse DNA. The resulting plasmid therefore contains a neo^r gene within the mouse genomic DNA sequences, all of which are positioned within a thymidine kinase encoding region. Plasmid construction in this manner is required to favor homologous recombination over random recombination [Chisaka, *et al.*, *Nature* *355*:516-520 (1992)].

verified with the primers set out in SEQ ID NOS: 50 and 51, which amplify from base 100 to 1405 after the initiating methionine.

Example 23

Construction of a Knock-out Mouse

In order to more accurately assess the immunological role of the protein encoded by the putative mouse α_d cDNA, a "knock-out" mouse is designed wherein the genomic DNA sequence encoding the putative α_d homolog is disrupted by homologous recombination. The significance of the protein encoded by the disrupted gene is thereby assessed by the absence of the encoded protein. Generation of "knock-out" mice is described in Deng, *et al.*, *Mol.Cell.Biol. 13*:2134-2140 (1993).

Design of such a mouse begins with construction of a plasmid containing sequences to be "knocked out" by homologous recombination events. A 750 base pair fragment of the mouse cDNA (corresponding to nucleotides 1985 to 2733 in SEQ ID NO: 45) was used to identify a mouse genomic sequence encoding the putative mouse α_d homolog from a λFIXII genomic library. Primary screening resulted in 14 positive plaques, seven of which were confirmed by secondary screening. Liquid lysates were obtained from two of the plaques giving the strongest signal and the λ DNA was isolated by conventional methods. Restriction mapping and Southern analysis confirmed the authenticity of one clone, designated 14-1, and the insert DNA was isolated by digestion with *Not*I. This fragment was cloned into Bluescript SKII$^+$.

In order to identify a restriction fragment of approximately 9 to 14 kb, a length reported to optimize the probability of homologous recombination events, Southern hybridization was performed with the 750 bp cDNA probe. Prior to hybridization, a restriction map was constructed for clone 14-1. A 12 kb fragment was identified as a possible candidate and this fragment was subcloned into pBluescript SKII$^+$ in a position wherein the mouse DNA is flanked by

10^6 dpm/ml. Hybridization was carried out at 42°C for 16-18 hours. Filters were washed extensively in 2X SSPE/0.1% SDS at room temperature and exposed to X-ray film to visualize any hybridizing plaques.

Two clones with significant sequence homology to human α_d were identified. Clone #2 was approximately 800 bp in length and mapped to the 5′ end of human α_d. Clone #2 includes an initiating methionine and complete leader sequence. Clone #7 was approximately 1.5 kb and includes an initiating methionine. The 5′ end of clone #7 overlapped that of clone #2, while the 3′ sequences terminated at a point beyond the I domain sequences. Internal sequencing of clone #7 is performed using the nested deletions sequencing technique.

The predicted N terminal amino acid sequence for rabbit α_d as determined from clones #2 and #7 indicated a protein with 73% identity with human α_d , 65% identity with mouse α_d, and 58% identity with mouse CD11b, human CD11b, and human CD11c. The nucleic acid sequence for clone #2 is set out in SEQ ID NO: 92; the predicted amino acid sequence is set out in SEQ ID NO: 93

Isolation of a full length rabbit α_d cDNA is carried out using labeled rabbit fragment, clone # 7, and rescreening the cDNA library from which the fragment was derived.

Isolation of a rabbit α_d clone allows expression of the protein, either on the surface of transfectants or as a soluble full length or truncated form. This protein is then used as an immunogen for the production of monoclonal antibodies for use in rabbit models of human disease states.

Example 24

Cloning of Rabbit α_d - Construction and Screening of the Rabbit cDNA Library

Identification of human α_d homologs in rats and mice led to the investigation of the existence of a rabbit homolog which would be useful in rabbit models of human disease states described *infra*.

Poly A^+ RNA was prepared from a whole rabbit spleen using an Invitrogen FastTrack kit (San Diego, CA) according to manufacturer's suggested protocol and reagents supplied with the kit. From 1.65 g tissue, 73 μg poly A^+RNA were isolated. The rabbit spleen RNA was used to construct a ZAP Express cDNA library using a kit from Stratagene (La Jolla, CA). Resulting cDNA was directionally cloned into *Eco*RI and *Xho*I sites in the lambda arms of a pBK-CMV phagemid vector. Gigapack II Gold (Stratagene) was used to package the lambda arms into phage particles. The resulting library titer was estimated to be approximately 8 x 10^5 particles, with an average insert size of 1.2 kb.

The library was amplified once by plating for confluent plaque growth and cell lysate was collected. The amplified library was plated at approximately 30,000 plaque forming units (pfu) per 150 mm plate with *E. coli* and the resulting mixture incubated for 12-16 hrs at 37°C to allow plaque formation. Phage DNA was transferred onto Hybond N^+ nylon membranes (Amersham, Arlington Heights, Illinois). The membranes were hybridized with a mixture of two random primed radiolabeled mouse α_d PCR DNA probes. The first probe was generated from a PCR product spanning nucleotides 149-946 in SEQ ID NO: 52. The second probe was from a PCR product spanning nucleotides 2752-3651 in SEQ ID NO: 52. Probes were labeled by random priming (Boehringer Mannheim Random Primed DNA Labeling Kit) and the reaction mixture was passed over a Sephadex G-50 column to remove unincorporated nucleotides. The hybridization solution was composed of 5X SSPE, 5X Denhardts, 1% SDS, 40% Formamide and the labeled probes at 1 x

functions which damage normal host tissue through either specific autoimmune responses or as a result of bystander cell damage.

Disease states in which there is evidence of macrophages playing a significant role in the disease process include multiple sclerosis, arthritis, graft atherosclerosis, some forms of diabetes and inflammatory bowel disease. Animal models, discussed below, have been shown to reproduce many of the aspects of these human disorders. Inhibitors of α_d function are tested in these model systems to determine if the potential exists for treating the corresponding human diseases.

A. Graft Arteriosclerosis

Cardiac transplantation is now the accepted form of therapeutic intervention for some types of end-state heart disease. As the use of cyclosporin A has increased one year survival rates to 80%, the development of progressive graft arteriosclerosis has emerged as the leading cause of death in cardiac transplants surviving beyond the first year. Recent studies have found that the incidence of significant graft arteriosclerosis 3 years following a cardiac transplant is in the range of 36-44% [Adams, *et al.*, *Transplantation 53*:1115-1119 (1992); Adams, *et al.*, *Transplantation 56*:794-799 (1993)].

Graft arteriosclerosis typically consists of diffuse, occlusive, intimal lesions which affect the entire coronary vessel wall, and are often accompanied by lipid deposition. While the pathogenesis of graft arteriosclerosis remains unknown, it is presumably linked to histocompatibility differences between donor and recipient, and is immunologic in nature. Histologically, the areas of intimal thickening are composed primarily of macrophages, although T cells are occasionally seen. It is therefore possible that macrophages expressing α_d may play a significant role in the induction and/or development of graft arteriosclerosis. In such a case, monoclonal antibodies or small molecule inhibitors (for example, soluble ICAM-R) of α_d function could be given

Example 25

Animal Models For Determining α_d Therapeutic Utility

Immunohistologic data in dog and *in situ* hybridization in rats and mice has determined that in spleen α_d is expressed primarily by macrophages present in red pulp and in lymph nodes, α_d is found in medullary cords and sinuses. The expression pattern is remarkably similar to what has been reported for two murine antigens defined by the monoclonal antibodies F4/80 and SK39. While biochemical characterization of these murine antigens has demonstrated that they are distinct from α_d, it is highly probably that α_d defines the same macrophage subset as the murine F4/80 and SK39 antigens.

In mouse, SK39-positive macrophages have been identified in splenic red pulp where they may participate in the clearance of foreign materials from circulation, and in medulla of lymph nodes [Jutila, *et al., J.Leukocyte Biol. 54*:30-39 (1993)]. SK39-positive macrophages have also been reported at sites of both acute and chronic inflammation. Furthermore, monocytes recruited to thioglycolate-inflamed peritoneal cavities also express the SK39 antigen. Collectively, these findings suggest that, if $SK39^+$ cells are also $\alpha_d{}^+$, then these cells are responsible for the clearance of foreign materials in the spleen and participate in inflammation where macrophages play a significant role.

While the function of α_d remains unclear, other more well characterized β_2 integrins have been shown to participate in a wide variety of adhesion events that facilitate cell migration, enhance phagocytosis, and promote cell-cell interactions, events which all lead to upregulation of inflammatory processes. Therefore, it is highly plausible that interfering with the normal α_d function may also interfere with inflammation where macrophages play a significant role. Such an anti-inflammatory effect could result from: i) blocking macrophage recruitment to sites of inflammation, ii) preventing macrophage activation at the site of inflammation or iii) interfering with macrophage effector

lumenal surface of the ascending aorta [Rosenfeld, *et al.*, *Arteriosclerosis* 7:9-23 (1987); Rosenfeld, *et al.*, *Arteriosclerosis* 7:24-34 (1987)]. The atherosclerotic lesions seen in these rabbits are simmer to those in humans. Lesions contain large numbers of T cells, most of which express CD45RO, a marker associated with memory T cells. Approximately half of the infiltrating T cells also express MHC class II antigen and some express the IL-2 receptor suggesting that many of the cells are in an activated state.

One feature of the atherosclerotic lesions found in cholesterol fed rabbits, but apparently absent in rodent models, is the accumulation of foam cell-rich lesions. Foam cell macrophages are believed to result from the uptake of oxidized low-density lipoprotein (LDL) by specific receptors. Oxidized LDL particles have been found to be toxic for some cell types including endothelial cells and smooth muscle cells. The uptake of potentially toxic, oxidized LDL particles by macrophages serves as an irritant and drives macrophage activation, contributing to the inflammation associated with atherosclerotic lesions.

Once monoclonal antibodies have been generated to rabbit α_d, cholesterol fed rabbits are treated. Treatments include prophylactic administration of α_d monoclonal antibodies or small molecule inhibitors, to demonstrate that α_d^+ macrophages are involved in the disease process. Additional studies would demonstrate that monoclonal antibodies to α_d or small molecule inhibitors are capable of reversing vessel damage detected in rabbits fed an atherogenic diet.

C. Insulin-dependent Diabetes

BB rats spontaneously develop insulin-dependent diabetes at 70-150 days of age. Using immunohistochemistry, MHC class II^+, $ED1^+$ macrophages can be detected infiltrating the islets early in the disease. Many of the macrophages appear to be engaged in phagocytosis of cell debris or normal cells. As the disease progresses, larger numbers of macrophages are found infiltrating

prophylactically to individuals who received heart transplants and are at risk of developing graft arteriosclerosis.

Although atherosclerosis in heart transplants presents the greatest threat to life, graft arteriosclerosis is also seen in other solid organ transplants, including kidneys and livers. Therapeutic use of α_d blocking agents could prevent graft arteriosclerosis in other organ transplants and reduce complications resulting from graft failure.

One model for graft arteriosclerosis in the rat involves heterotopic cardiac allografts transplanted across minor histocompatibility barriers. When Lewis cardiac allografts are transplanted into MHC class I and II compatible F-344 recipients, 80% of the allografts survive at least 3 weeks, while 25% of the grafts survive indefinitely. During this low-grade graft rejection, arteriosclerosis lesions form in the donor heart. Arterial lesions in 120 day old allografts typically have diffuse fibrotic intimal thickening indistinguishable in appearance from graft arteriosclerosis lesions found in rejecting human cardiac allografts.

Rats are transplanted with hearts mismatched at minor histocompatibility antigens, for example Lewis into F-344. Monoclonal antibodies specific for rat α_d or small molecule inhibitors of α_d are given periodically to transplant recipients. Treatment is expected to reduce the incidence of graft arteriosclerosis in non-rejecting donor hearts. Treatment of rats with α_d monoclonal antibodies or small molecule inhibitors may not be limited to prophylactic treatments. Blocking α_d function is also be expected to reduce macrophage mediated inflammation and allow reversal of arterial damage in the graft.

B. Atherosclerosis in Rabbits Fed Cholesterol

Rabbits fed an atherogenic diet containing a cholesterol supplement for approximately 12-16 weeks develop intimal lesions that cover most of the

the islets, although significant numbers of T cells, and later B cells, also appear to be recruited to the site [Hanenberg, *et al.*, *Diabetologia 32*:126-134 (1989)].

Development of diabetes in BB rats appears to depend on both early macrophage infiltration and subsequent T cells recruitment. Treatment of BB rats with silica particles, which are toxic to macrophages, has been effective in blocking the early macrophage infiltration of the islets. In the absence of early macrophage infiltration, subsequent tissue damage by an autoaggressive lymphocyte population fails to occur. Administration of monoclonal antibody OX-19 (specific for rat CD5) or monoclonal antibody OX-8 (specific for rat CD8), which block the T cell-associated phase of the disease, is also effective in suppressing the development of diabetes.

The central role of macrophages in the pathology of this model makes it attractive for testing inhibitors of α_d function. Rats genetically predisposed to the development of insulin-dependent diabetes are treated with monoclonal antibodies to α_d or small molecule inhibitors and evaluated for the development of the disease. Preventing or delaying clinical onset is evidence that α_d plays a pivotal role in macrophage damage to the islet cells.

D. Inflammatory Bowel Disease (Crohn's Disease, Ulcerative Colitis)

Animal models used in the study of inflammatory bowel disease (IBD) are generally elicited by intrarectal administration of noxious irritants (e.g. acetic acid or trinitrobenzene sulfonic acid/ethanol). Colonic inflammation induced by these agents is the result of chemical or metabolic injury and lacks the chronic and spontaneously relapsing inflammation associated with human IBD. However, a recently described model using subserosal injections of purified peptidoglycan-polysaccharide (PG-PS) polymers from either group A or group D streptococci appears to be a more physiologically relevant model for human IBD [Yamada, *et al.*, *Gastroenterolgy 104*:759-771 (1993)].

In this model PG-PS is injected into the subserosal layer of the distal colon. The resulting inflammatory response is biphasic with an initial acute episode three days after injection, which is followed by a spontaneous chronic phase three to four weeks later. The late phase response is granulomatous in nature, and results in colonic thickening, adhesions, colonic nodules and mucosal lesions. In addition to mucosal injury, PG-PS colitis frequently leads to arthritis anemia and granulomatous hepatitis. The extraintestinal manifestations of the disease make the model attractive for studying Crohn's colitis in that a significant number of patients with active Crohn's disease suffer from arthritic joint disease and hepatobillary inflammation.

Granulomatous lesions are the result of chronic inflammation which leads to the recruitment and subsequent activation of cells of the monocyte/macrophage lineage. Presence of granulomatous lesions in Crohn's disease and the above animal model make this an attractive clinical target for α_d monoclonal antibodies or other inhibitors of α_d function. Inhibitors of α_d function are expected to block the formation of lesions associated with IBD or even reverse tissue damage seen in the disease.

E. Arthritis

Arthritis appears to be a multi-factorial disease process involving a variety of inflammatory cell types including neutrophils, T lymphocytes and phagocytic macrophages. Although a variety of arthritis models exist, preparations of streptococcal cell wall proteoglycan produce a disorder most similar to the human disease.

In rats, streptococcal cell wall induces inflammation of peripheral joints characterized by repeated episodes of disease progression followed by remission and eventually resulting in joint destruction over a period of several months [Cromartie, *et al., J.Exp.Med. 146*:1585-1602 (1977); Schwab *et al., Infection and Immunity 59*:4436-4442 (1991)]. During the chronic phase of the

disease, mononuclear phagocytes or macrophages are believed to play a major role in destruction of the synovium. Furthermore, agents which suppress the recruitment of macrophages into the synovium effectively reduce the inflammation and pathology characteristic of arthritis.

A central role for the macrophage in synovium destruction that leads to arthritis predicts that monoclonal antibodies to α_d or inhibitors of α_d function may have therapeutic potential in the treatment of this disease. As in other models previously described, α_d monoclonal antibodies or small molecule inhibitors administered prophylactically are expected to block or moderate joint inflammation and prevent destruction of the synovium. Agents that interfere with α_d function may also moderate ongoing inflammation by preventing the recruitment of additional macrophages to the joint or blocking macrophage activation. The net result would be to reverse ongoing destruction of the joint and facilitate tissue repair.

F. Multiple Sclerosis

Although pathogenesis of multiple sclerosis (MS) remains unclear, it is generally accepted that the disease is mediated by $CD4^+$ T cells which recognize autoantigens in the central nervous system and initiate an inflammatory cascade. The resulting immune response results in the recruitment of additional inflammatory cells, including activated macrophages which contribute to the disease. Experimental autoimmune encephalomyelitis (EAE) is an animal model which reproduces some aspects of MS. Recently, monoclonal antibodies reactive with CD11b/CD18 [Huitinga, *et al.*, *Eur.J.Immunol.* *23*:709-715 (1993)] present on inflammatory macrophages have been shown to block both clinical and histologic disease. The results suggest that monoclonal antibodies or small molecule inhibitors to α_d are likely to be effective in blocking the inflammatory response in EAE. Such agents also have important therapeutic applications in the treatment of MS.

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

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THE INTERNATIONAL APPLICATION

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..3485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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   Thr Phe Gly Thr Val Leu Leu Leu Ser Val Leu Ala Ser Tyr His
    1               5                  10                  15

GGA TTC AAC CTG GAT GTG GAG GAG CCT ACG ATC TTC CAG GAG GAT GCA          95
Gly Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala
                20                  25                  30

GGC GGC TTT GGG CAG AGC GTG GTG CAG TTC GGT GGA TCT CGA CTC GTG         143
Gly Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val
            35                  40                  45

GTG GGA GCA CCC CTG GAG GTG GTG GCG GCC AAC CAG ACG GGA CGG CTG         191
Val Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu
        50                  55                  60

TAT GAC TGC GCA GCT GCC ACC GGC ATG TGC CAG CCC ATC CCG CTG CAC         239
Tyr Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His
    65                  70                  75

ATC CGC CCT GAG GCC GTG AAC ATG TCC TTG GGC CTG ACC CTG GCA GCC         287
Ile Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala
80                  85                  90                  95

TCC ACC AAC GGC TCC CGG CTC CTG GCC TGT GGC CCG ACC CTG CAC AGA         335
Ser Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg
                100                 105                 110

GTC TGT GGG GAG AAC TCA TAC TCA AAG GGT TCC TGC CTC CTG CTG GGC         383
Val Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Leu Gly
            115                 120                 125

TCG CGC TGG GAG ATC ATC CAG ACA GTC CCC GAC GCC ACG CCA GAG TGT         431
Ser Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys
        130                 135                 140

CCA CAT CAA GAG ATG GAC ATC GTC TTC CTG ATT GAC GGC TCT GGA AGC         479
Pro His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser
    145                 150                 155

ATT GAC CAA AAT GAC TTT AAC CAG ATG AAG GGC TTT GTC CAA GCT GTC         527
Ile Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val
160                 165                 170                 175

ATG GGC CAG TTT GAG GGC ACT GAC ACC CTG TTT GCA CTG ATG CAG TAC         575
Met Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr
                180                 185                 190

TCA AAC CTC CTG AAG ATC CAC TTC ACC TTC ACC CAA TTC CGG ACC AGC         623
Ser Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser
            195                 200                 205

CCG AGC CAG CAG AGC CTG GTG GAT CCC ATC GTC CAA CTG AAA GGC CTG         671
Pro Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu
        210                 215                 220
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ACG TTC ACG GCC ACG GGC ATC CTG ACA GTG GTG ACA CAG CTA TTT CAT          719
Thr Phe Thr Ala Thr Gly Ile Leu Thr Val Val Thr Gln Leu Phe His
    225                 230                 235

CAT AAG AAT GGG GCC CGA AAA AGT GCC AAG AAG ATC CTC ATT GTC ATC          767
His Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile
240                 245                 250                 255

ACA GAT GGG CAG AAG TAC AAA GAC CCC CTG GAA TAC AGT GAT GTC ATC          815
Thr Asp Gly Gln Lys Tyr Lys Asp Pro Leu Glu Tyr Ser Asp Val Ile
                260                 265                 270

CCC CAG GCA GAG AAG GCT GGC ATC ATC CGC TAC GCT ATC GGG GTG GGA          863
Pro Gln Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly
            275                 280                 285

CAC GCT TTC CAG GGA CCC ACT GCC AGG CAG GAG CTG AAT ACC ATC AGC          911
His Ala Phe Gln Gly Pro Thr Ala Arg Gln Glu Leu Asn Thr Ile Ser
        290                 295                 300

TCA GCG CCT CCG CAG GAC CAC GTG TTC AAG GTG GAC AAC TTT GCA GCC          959
Ser Ala Pro Pro Gln Asp His Val Phe Lys Val Asp Asn Phe Ala Ala
    305                 310                 315

CTT GGC AGC ATC CAG AAG CAG CTG CAG GAG AAG ATC TAT GCA GTT GAG         1007
Leu Gly Ser Ile Gln Lys Gln Leu Gln Glu Lys Ile Tyr Ala Val Glu
320                 325                 330                 335

GGA ACC CAG TCC AGG GCA AGC AGC TCC TTC CAG CAC GAG ATG TCC CAA         1055
Gly Thr Gln Ser Arg Ala Ser Ser Ser Phe Gln His Glu Met Ser Gln
                340                 345                 350

GAA GGC TTC AGC ACA GCC CTC ACA ATG GAT GGC CTC TTC CTG GGG GCT         1103
Glu Gly Phe Ser Thr Ala Leu Thr Met Asp Gly Leu Phe Leu Gly Ala
            355                 360                 365

GTG GGG AGC TTT AGC TGG TCT GGA GGT GCC TTC CTG TAT CCC CCA AAT         1151
Val Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn
        370                 375                 380

ATG AGC CCC ACC TTC ATC AAC ATG TCT CAG GAG AAT GTG GAC ATG AGG         1199
Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg
    385                 390                 395

GAC TCT TAC CTG GGT TAC TCC ACC GAG CTA GCC CTG TGG AAG GGG GTA         1247
Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly Val
400                 405                 410                 415

CAG AAC CTG GTC CTG GGG GCC CCC CGC TAC CAG CAT ACC GGG AAG GCT         1295
Gln Asn Leu Val Leu Gly Ala Pro Arg Tyr Gln His Thr Gly Lys Ala
                420                 425                 430

GTC ATC TTC ACC CAG GTG TCC AGG CAA TGG AGG AAG AAG GCC GAA GTC         1343
Val Ile Phe Thr Gln Val Ser Arg Gln Trp Arg Lys Lys Ala Glu Val
            435                 440                 445

ACA GGG ACG CAG ATC GGC TCC TAC TTC GGG GCC TCC CTC TGC TCC GTG         1391
Thr Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val
        450                 455                 460
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GAT GTG GAC AGC GAT GGC AGC ACC GAC CTG ATC CTC ATT GGG GCC CCC      1439
Asp Val Asp Ser Asp Gly Ser Thr Asp Leu Ile Leu Ile Gly Ala Pro
    465                 470                 475

CAT TAC TAT GAG CAG ACC CGA GGG GGC CAG GTG TCC GTG TGT CCC TTG      1487
His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
480                 485                 490                 495

CCT AGG GGG CAG AGG GTG CAG TGG CAG TGT GAC GCT GTT CTC CGT GGT      1535
Pro Arg Gly Gln Arg Val Gln Trp Gln Cys Asp Ala Val Leu Arg Gly
                500                 505                 510

GAG CAG GGC CAC CCC TGG GGC CGC TTT GGG GCA GCC CTG ACA GTG TTG      1583
Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
            515                 520                 525

GGG GAT GTG AAT GAG GAC AAG CTG ATA GAC GTG GCC ATT GGG GCC CCG      1631
Gly Asp Val Asn Glu Asp Lys Leu Ile Asp Val Ala Ile Gly Ala Pro
        530                 535                 540

GGA GAG CAG GAG AAC CGG GGT GCT GTC TAC CTG TTT CAC GGA GCC TCA      1679
Gly Glu Gln Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Ala Ser
    545                 550                 555

GAA TCC GGC ATC AGC CCC TCC CAC AGC CAG CGG ATT GCC AGC TCC CAG      1727
Glu Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Ser Ser Gln
560                 565                 570                 575

CTC TCC CCC AGG CTG CAG TAT TTT GGG CAG GCG CTG AGT GGG GGT CAG      1775
Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln
                580                 585                 590

GAC CTC ACC CAG GAT GGA CTG ATG GAC CTG GCC GTG GGG GCC CGG GGC      1823
Asp Leu Thr Gln Asp Gly Leu Met Asp Leu Ala Val Gly Ala Arg Gly
            595                 600                 605

CAG GTG CTC CTG CTC AGG AGT CTG CCG GTG CTG AAA GTG GGG GTG GCC      1871
Gln Val Leu Leu Leu Arg Ser Leu Pro Val Leu Lys Val Gly Val Ala
        610                 615                 620

ATG AGA TTC AGC CCT GTG GAG GTG GCC AAG GCT GTG TAC CGG TGC TGG      1919
Met Arg Phe Ser Pro Val Glu Val Ala Lys Ala Val Tyr Arg Cys Trp
    625                 630                 635

GAA GAG AAG CCC AGT GCC CTG GAA GCT GGG GAC GCC ACC GTC TGT CTC      1967
Glu Glu Lys Pro Ser Ala Leu Glu Ala Gly Asp Ala Thr Val Cys Leu
640                 645                 650                 655

ACC ATC CAG AAA AGC TCA CTG GAC CAG CTA GGT GAC ATC CAA AGC TCT      2015
Thr Ile Gln Lys Ser Ser Leu Asp Gln Leu Gly Asp Ile Gln Ser Ser
                660                 665                 670

GTC AGG TTT GAT CTG GCA CTG GAC CCA GGT CGT CTG ACT TCT CGT GCC      2063
Val Arg Phe Asp Leu Ala Leu Asp Pro Gly Arg Leu Thr Ser Arg Ala
            675                 680                 685

ATT TTC AAT GAA ACC AAG AAC CCC ACT TTG ACT CGA AGA AAA ACC CTG      2111
Ile Phe Asn Glu Thr Lys Asn Pro Thr Leu Thr Arg Arg Lys Thr Leu
        690                 695                 700
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GGA CTG GGG ATT CAC TGT GAA ACC CTG AAG CTG CTT TTG CCA GAT TGT          2159
Gly Leu Gly Ile His Cys Glu Thr Leu Lys Leu Leu Leu Pro Asp Cys
    705                 710                 715

GTG GAG GAT GTG GTG AGC CCC ATC ATT CTG CAC CTC AAC TTC TCA CTG          2207
Val Glu Asp Val Val Ser Pro Ile Ile Leu His Leu Asn Phe Ser Leu
720                 725                 730                 735

GTG AGA GAG CCC ATC CCC TCC CCC CAG AAC CTG CGT CCT GTG CTG GCC          2255
Val Arg Glu Pro Ile Pro Ser Pro Gln Asn Leu Arg Pro Val Leu Ala
                740                 745                 750

GTG GGC TCA CAA GAC CTC TTC ACT GCT TCT CTC CCC TTC GAG AAG AAC          2303
Val Gly Ser Gln Asp Leu Phe Thr Ala Ser Leu Pro Phe Glu Lys Asn
            755                 760                 765

TGT GGG CAA GAT GGC CTC TGT GAA GGG GAC CTG GGT GTC ACC CTC AGC          2351
Cys Gly Gln Asp Gly Leu Cys Glu Gly Asp Leu Gly Val Thr Leu Ser
        770                 775                 780

TTC TCA GGC CTG CAG ACC CTG ACC GTG GGG AGC TCC CTG GAG CTC AAC          2399
Phe Ser Gly Leu Gln Thr Leu Thr Val Gly Ser Ser Leu Glu Leu Asn
    785                 790                 795

GTG ATT GTG ACT GTG TGG AAC GCA GGT GAG GAT TCC TAC GGA ACC GTG          2447
Val Ile Val Thr Val Trp Asn Ala Gly Glu Asp Ser Tyr Gly Thr Val
800                 805                 810                 815

GTC AGC CTC TAC TAT CCA GCA GGG CTG TCG CAC CGA CGG GTG TCA GGA          2495
Val Ser Leu Tyr Tyr Pro Ala Gly Leu Ser His Arg Arg Val Ser Gly
                820                 825                 830

GCC CAG AAG CAG CCC CAT CAG AGT GCC CTG CGC CTG GCA TGT GAG ACA          2543
Ala Gln Lys Gln Pro His Gln Ser Ala Leu Arg Leu Ala Cys Glu Thr
            835                 840                 845

GTG CCC ACT GAG GAT GAG GGC CTA AGA AGC AGC CGC TGC AGT GTC AAC          2591
Val Pro Thr Glu Asp Glu Gly Leu Arg Ser Ser Arg Cys Ser Val Asn
        850                 855                 860

CAC CCC ATC TTC CAT GAG GGC TCT AAC GGC ACC TTC ATA GTC ACA TTC          2639
His Pro Ile Phe His Glu Gly Ser Asn Gly Thr Phe Ile Val Thr Phe
    865                 870                 875

GAT GTC TCC TAC AAG GCC ACC CTG GGA GAC AGG ATG CTT ATG AGG GCC          2687
Asp Val Ser Tyr Lys Ala Thr Leu Gly Asp Arg Met Leu Met Arg Ala
880                 885                 890                 895

AGT GCA AGC AGT GAG AAC AAT AAG GCT TCA AGC AGC AAG GCC ACC TTC          2735
Ser Ala Ser Ser Glu Asn Asn Lys Ala Ser Ser Ser Lys Ala Thr Phe
                900                 905                 910

CAG CTG GAG CTC CCG GTG AAG TAT GCA GTC TAC ACC ATG ATC AGC AGG          2783
Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Thr Met Ile Ser Arg
            915                 920                 925

CAG GAA GAA TCC ACC AAG TAC TTC AAC TTT GCA ACC TCC GAT GAG AAG          2831
Gln Glu Glu Ser Thr Lys Tyr Phe Asn Phe Ala Thr Ser Asp Glu Lys
        930                 935                 940
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AAA ATG AAA GAG GCT GAG CAT CGA TAC CGT GTG AAT AAC CTC AGC CAG      2879
Lys Met Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Gln
    945                 950                 955

CGA GAT CTG GCC ATC AGC ATT AAC TTC TGG GTT CCT GTC CTG CTG AAC      2927
Arg Asp Leu Ala Ile Ser Ile Asn Phe Trp Val Pro Val Leu Leu Asn
960                 965                 970                 975

GGG GTG GCT GTG TGG GAT GTG GTC ATG GAG GCC CCA TCT CAG AGT CTC      2975
Gly Val Ala Val Trp Asp Val Val Met Glu Ala Pro Ser Gln Ser Leu
                980                 985                 990

CCC TGT GTT TCA GAG AGA AAA CCT CCC CAG CAT TCT GAC TTC CTG ACC      3023
Pro Cys Val Ser Glu Arg Lys Pro Pro Gln His Ser Asp Phe Leu Thr
            995                 1000                1005

CAG ATT TCA AGA AGT CCC ATG CTG GAC TGC TCC ATT GCT GAC TGC CTG      3071
Gln Ile Ser Arg Ser Pro Met Leu Asp Cys Ser Ile Ala Asp Cys Leu
        1010                1015                1020

CAG TTC CGC TGT GAC GTC CCC TCC TTC AGC GTC CAG GAG GAG CTG GAT      3119
Gln Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu Leu Asp
    1025                1030                1035

TTC ACC CTG AAG GGC AAT CTC AGT TTC GGC TGG GTC CGC GAG ACA TTG      3167
Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val Arg Glu Thr Leu
1040                1045                1050                1055

CAG AAG AAG GTG TTG GTC GTG AGT GTG GCT GAA ATT ACG TTC GAC ACA      3215
Gln Lys Lys Val Leu Val Val Ser Val Ala Glu Ile Thr Phe Asp Thr
                1060                1065                1070

TCC GTG TAC TCC CAG CTT CCA GGA CAG GAG GCA TTT ATG AGA GCT CAG      3263
Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Met Arg Ala Gln
            1075                1080                1085

ATG GAG ATG GTG CTA GAA GAA GAC GAG GTC TAC AAT GCC ATT CCC ATC      3311
Met Glu Met Val Leu Glu Glu Asp Glu Val Tyr Asn Ala Ile Pro Ile
        1090                1095                1100

ATC ATG GGC AGC TCT GTG GGG GCT CTG CTA CTG CTG GCG CTC ATC ACA      3359
Ile Met Gly Ser Ser Val Gly Ala Leu Leu Leu Leu Ala Leu Ile Thr
    1105                1110                1115

GCC ACA CTG TAC AAG CTT GGC TTC TTC AAA CGC CAC TAC AAG GAA ATG      3407
Ala Thr Leu Tyr Lys Leu Gly Phe Phe Lys Arg His Tyr Lys Glu Met
1120                1125                1130                1135

CTG GAG GAC AAG CCT GAA GAC ACT GCC ACA TTC AGT GGG GAC GAT TTC      3455
Leu Glu Asp Lys Pro Glu Asp Thr Ala Thr Phe Ser Gly Asp Asp Phe
                1140                1145                1150

AGC TGT GTG GCC CCA AAT GTG CCT TTG TCC TAATAATCCA CTTTCCTGTT        3505
Ser Cys Val Ala Pro Asn Val Pro Leu Ser
            1155                1160

TATCTCTACC ACTGTGGGCT GGACTTGCTT GCAACCATAA ATCAACTTAC ATGGAAACAA    3566

CTTCTGCATA GATCTGCACT GGCCTAAGCA ACCTACCAGG TGCTAAGCAC CTTCTCGGAG    3625

AGATAGAGAT TGTAATGTTT TTACATATCT GTCCATCTTT TTCAGCAATG ACCCACTTTT    3685
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TACAGAAGCA GGCATGGTGC CAGCATAAAT TTTCATATGC T 3726

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Phe Gly Thr Val Leu Leu Leu Ser Val Leu Ala Ser Tyr His Gly
1 5 10 15

Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala Gly
20 25 30

Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val Val
35 40 45

Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu Tyr
50 55 60

Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His Ile
65 70 75 80

Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala Ser
85 90 95

Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg Val
100 105 110

Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Leu Gly Ser
115 120 125

Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys Pro
130 135 140

His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile
145 150 155 160

Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val Met
165 170 175

Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr Ser
180 185 190

Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser Pro
195 200 205

Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu Thr
210 215 220

Phe Thr Ala Thr Gly Ile Leu Thr Val Val Thr Gln Leu Phe His His
225 230 235 240

Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile Thr
245 250 255

```
Asp Gly Gln Lys Tyr Lys Asp Pro Leu Glu Tyr Ser Asp Val Ile Pro
            260                 265                 270

Gln Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly His
        275                 280                 285

Ala Phe Gln Gly Pro Thr Ala Arg Gln Glu Leu Asn Thr Ile Ser Ser
    290                 295                 300

Ala Pro Pro Gln Asp His Val Phe Lys Val Asp Asn Phe Ala Ala Leu
305                 310                 315                 320

Gly Ser Ile Gln Lys Gln Leu Gln Glu Lys Ile Tyr Ala Val Glu Gly
                325                 330                 335

Thr Gln Ser Arg Ala Ser Ser Ser Phe Gln His Glu Met Ser Gln Glu
            340                 345                 350

Gly Phe Ser Thr Ala Leu Thr Met Asp Gly Leu Phe Leu Gly Ala Val
        355                 360                 365

Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn Met
    370                 375                 380

Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg Asp
385                 390                 395                 400

Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly Val Gln
                405                 410                 415

Asn Leu Val Leu Gly Ala Pro Arg Tyr Gln His Thr Gly Lys Ala Val
            420                 425                 430

Ile Phe Thr Gln Val Ser Arg Gln Trp Arg Lys Lys Ala Glu Val Thr
        435                 440                 445

Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val Asp
    450                 455                 460

Val Asp Ser Asp Gly Ser Thr Asp Leu Ile Leu Ile Gly Ala Pro His
465                 470                 475                 480

Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu Pro
                485                 490                 495

Arg Gly Gln Arg Val Gln Trp Gln Cys Asp Ala Val Leu Arg Gly Glu
            500                 505                 510

Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu Gly
        515                 520                 525

Asp Val Asn Glu Asp Lys Leu Ile Asp Val Ala Ile Gly Ala Pro Gly
    530                 535                 540

Glu Gln Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Ala Ser Glu
545                 550                 555                 560

Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Ser Ser Gln Leu
                565                 570                 575
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Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln Asp
580 585 590

Leu Thr Gln Asp Gly Leu Met Asp Leu Ala Val Gly Ala Arg Gly Gln
595 600 605

Val Leu Leu Leu Arg Ser Leu Pro Val Leu Lys Val Gly Val Ala Met
610 615 620

Arg Phe Ser Pro Val Glu Val Ala Lys Ala Val Tyr Arg Cys Trp Glu
625 630 635 640

Glu Lys Pro Ser Ala Leu Glu Ala Gly Asp Ala Thr Val Cys Leu Thr
645 650 655

Ile Gln Lys Ser Ser Leu Asp Gln Leu Gly Asp Ile Gln Ser Ser Val
660 665 670

Arg Phe Asp Leu Ala Leu Asp Pro Gly Arg Leu Thr Ser Arg Ala Ile
675 680 685

Phe Asn Glu Thr Lys Asn Pro Thr Leu Thr Arg Arg Lys Thr Leu Gly
690 695 700

Leu Gly Ile His Cys Glu Thr Leu Lys Leu Leu Leu Pro Asp Cys Val
705 710 715 720

Glu Asp Val Val Ser Pro Ile Ile Leu His Leu Asn Phe Ser Leu Val
725 730 735

Arg Glu Pro Ile Pro Ser Pro Gln Asn Leu Arg Pro Val Leu Ala Val
740 745 750

Gly Ser Gln Asp Leu Phe Thr Ala Ser Leu Pro Phe Glu Lys Asn Cys
755 760 765

Gly Gln Asp Gly Leu Cys Glu Gly Asp Leu Gly Val Thr Leu Ser Phe
770 775 780

Ser Gly Leu Gln Thr Leu Thr Val Gly Ser Ser Leu Glu Leu Asn Val
785 790 795 800

Ile Val Thr Val Trp Asn Ala Gly Glu Asp Ser Tyr Gly Thr Val Val
805 810 815

Ser Leu Tyr Tyr Pro Ala Gly Leu Ser His Arg Arg Val Ser Gly Ala
820 825 830

Gln Lys Gln Pro His Gln Ser Ala Leu Arg Leu Ala Cys Glu Thr Val
835 840 845

Pro Thr Glu Asp Glu Gly Leu Arg Ser Ser Arg Cys Ser Val Asn His
850 855 860

Pro Ile Phe His Glu Gly Ser Asn Gly Thr Phe Ile Val Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Thr Leu Gly Asp Arg Met Leu Met Arg Ala Ser
885 890 895

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Ala Ser Ser Glu Asn Asn Lys Ala Ser Ser Ser Lys Ala Thr Phe Gln
            900                 905                 910

Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Thr Met Ile Ser Arg Gln
        915                 920                 925

Glu Glu Ser Thr Lys Tyr Phe Asn Phe Ala Thr Ser Asp Glu Lys Lys
    930                 935                 940

Met Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Gln Arg
945                 950                 955                 960

Asp Leu Ala Ile Ser Ile Asn Phe Trp Val Pro Val Leu Leu Asn Gly
                965                 970                 975

Val Ala Val Trp Asp Val Val Met Glu Ala Pro Ser Gln Ser Leu Pro
            980                 985                 990

Cys Val Ser Glu Arg Lys Pro Pro Gln His Ser Asp Phe Leu Thr Gln
        995                 1000                1005

Ile Ser Arg Ser Pro Met Leu Asp Cys Ser Ile Ala Asp Cys Leu Gln
    1010                1015                1020

Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln Glu Glu Leu Asp Phe
1025                1030                1035                1040

Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val Arg Glu Thr Leu Gln
                1045                1050                1055

Lys Lys Val Leu Val Val Ser Val Ala Glu Ile Thr Phe Asp Thr Ser
            1060                1065                1070

Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Met Arg Ala Gln Met
        1075                1080                1085

Glu Met Val Leu Glu Glu Asp Glu Val Tyr Asn Ala Ile Pro Ile Ile
    1090                1095                1100

Met Gly Ser Ser Val Gly Ala Leu Leu Leu Leu Ala Leu Ile Thr Ala
1105                1110                1115                1120

Thr Leu Tyr Lys Leu Gly Phe Phe Lys Arg His Tyr Lys Glu Met Leu
                1125                1130                1135

Glu Asp Lys Pro Glu Asp Thr Ala Thr Phe Ser Gly Asp Asp Phe Ser
            1140                1145                1150

Cys Val Ala Pro Asn Val Pro Lys Ser
        1155                1160
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ala Leu Arg Val Leu Leu Leu Thr Ala Leu Thr Leu Cys His Gly
1               5                  10                  15

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
            20                  25                  30

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
        35                  40                  45

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
    50                  55                  60

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
65                  70                  75                  80

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
                85                  90                  95

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
            100                 105                 110

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
        115                 120                 125

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
    130                 135                 140

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
145                 150                 155                 160

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
                165                 170                 175

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
            180                 185                 190

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
        195                 200                 205

Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
    210                 215                 220

Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
225                 230                 235                 240

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
                245                 250                 255

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
            260                 265                 270

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
        275                 280                 285

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
    290                 295                 300
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Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
305                 310                 315                 320

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
                325                 330                 335

Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
            340                 345                 350

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
        355                 360                 365

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
    370                 375                 380

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
385                 390                 395                 400

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
                405                 410                 415

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val
            420                 425                 430

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val
        435                 440                 445

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
    450                 455                 460

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
465                 470                 475                 480

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
                485                 490                 495

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
            500                 505                 510

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
        515                 520                 525

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
    530                 535                 540

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
545                 550                 555                 560

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
                565                 570                 575

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
            580                 585                 590

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
        595                 600                 605

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
    610                 615                 620
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Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
625 630 635 640

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
645 650 655

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
660 665 670

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
675 680 685

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
690 695 700

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
705 710 715 720

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
725 730 735

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
740 745 750

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
755 760 765

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
770 775 780

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
785 790 795 800

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
805 810 815

Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
820 825 830

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
835 840 845

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
850 855 860

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
865 870 875 880

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
885 890 895

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
900 905 910

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
915 920 925

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
930 935 940

```
Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
945                 950                 955                 960

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
                965                 970                 975

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
            980                 985                 990

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
        995                 1000                1005

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
    1010                1015                1020

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly Ile
1025                1030                1035                1040

Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe Asp Trp
                1045                1050                1055

Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser Thr Ala Glu
            1060                1065                1070

Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro Gly Gln Gly Ala
        1075                1080                1085

Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu Pro Phe Glu Val Pro
    1090                1095                1100

Asn Pro Leu Pro Leu Ile Val Gly Ser Ser Val Gly Gly Leu Leu Leu
1105                1110                1115                1120

Leu Ala Leu Ile Thr Ala Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg
                1125                1130                1135

Gln Tyr Lys Asp Met Met Ser Glu Gly Gly Pro Pro Gly Ala Glu Pro
            1140                1145                1150

Gln
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Thr Arg Thr Arg Ala Ala Leu Leu Leu Phe Thr Ala Leu Ala Thr
1               5                   10                  15

Ser Leu Gly Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Arg Val
            20                  25                  30
```

Asp Ser Ala Gly Phe Gly Asp Ser Val Val Gln Tyr Ala Asn Ser Trp
35 40 45

Val Val Val Gly Ala Pro Gln Lys Ile Ile Ala Ala Asn Gln Ile Gly
50 55 60

Gly Leu Tyr Gln Cys Gly Tyr Ser Thr Gly Ala Cys Glu Pro Ile Gly
65 70 75 80

Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85 90 95

Ala Ser Thr Thr Ser Pro Ser Gln Leu Leu Ala Cys Gly Pro Thr Val
100 105 110

His His Glu Cys Gly Arg Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu
115 120 125

Leu Gly Pro Thr Gln Leu Thr Gln Arg Leu Pro Val Ser Arg Gln Glu
130 135 140

Cys Pro Arg Gln Glu Gln Asp Ile Val Phe Leu Ile Asp Gly Ser Gly
145 150 155 160

Ser Ile Ser Ser Arg Asn Phe Ala Thr Met Met Asn Phe Val Arg Ala
165 170 175

Val Ile Ser Gln Phe Gln Arg Pro Ser Thr Gln Phe Ser Leu Met Gln
180 185 190

Phe Ser Asn Lys Phe Gln Thr His Phe Thr Phe Glu Glu Phe Arg Arg
195 200 205

Thr Ser Asn Pro Leu Ser Leu Leu Ala Ser Val His Gln Leu Gln Gly
210 215 220

Phe Thr Tyr Thr Ala Thr Ala Ile Gln Asn Val Val His Arg Leu Phe
225 230 235 240

His Ala Ser Tyr Gly Ala Arg Arg Asp Ala Ile Lys Ile Leu Ile Val
245 250 255

Ile Thr Asp Gly Lys Lys Glu Gly Asp Ser Leu Asp Tyr Lys Asp Val
260 265 270

Ile Pro Met Ala Asp Ala Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val
275 280 285

Gly Leu Ala Phe Gln Asn Arg Asn Ser Trp Lys Glu Leu Asn Asp Ile
290 295 300

Ala Ser Lys Pro Ser Gln Glu His Ile Phe Lys Val Glu Asp Phe Asp
305 310 315 320

Ala Leu Lys Asp Ile Gln Asn Gln Leu Lys Glu Lys Ile Phe Ala Ile
325 330 335

Glu Gly Thr Glu Thr Ile Ser Ser Ser Ser Phe Glu Leu Glu Met Ala
340 345 350

Gln Glu Gly Phe Ser Ala Val Phe Thr Pro Asp Gly Pro Val Leu Gly
355 360 365

Ala Val Gly Ser Phe Thr Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro
370 375 380

Asn Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met
385 390 395 400

Arg Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly
405 410 415

Val Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Lys
420 425 430

Ala Val Ile Phe Ile Gln Val Ser Arg Gln Trp Arg Met Lys Ala Glu
435 440 445

Val Ile Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser
450 455 460

Val Asp Val Asp Thr Asp Gly Ser Thr Asp Leu Val Leu Ile Gly Ala
465 470 475 480

Pro His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro
485 490 495

Leu Pro Arg Gly Trp Arg Arg Trp Trp Cys Asp Ala Val Leu Tyr Gly
500 505 510

Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
515 520 525

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Val Ile Gly Ala Pro
530 535 540

Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Val Leu
545 550 555 560

Gly Pro Ser Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Gln
565 570 575

Leu Ser Ser Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln
580 585 590

Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Arg Gly
595 600 605

Gln Val Leu Leu Leu Arg Thr Arg Pro Val Leu Trp Val Gly Val Ser
610 615 620

Met Gln Phe Ile Pro Ala Glu Ile Pro Arg Ser Ala Phe Glu Cys Arg
625 630 635 640

Glu Gln Val Val Ser Glu Gln Thr Leu Val Gln Ser Asn Ile Cys Leu
645 650 655

Tyr Ile Asp Lys Arg Ser Lys Asn Leu Leu Gly Ser Arg Asp Leu Gln
660 665 670

Ser Ser Val Thr Leu Asp Leu Ala Leu Ala Pro Gly Arg Leu Ser Pro
675 680 685

Arg Ala Ile Phe Gln Glu Thr Lys Asn Arg Ser Leu Ser Arg Val Arg
690 695 700

Val Leu Gly Leu Lys Ala His Cys Glu Asn Phe Asn Leu Leu Leu Pro
705 710 715 720

Ser Cys Val Glu Asp Ser Val Ile Pro Ile Ile Leu Arg Leu Asn Phe
725 730 735

Thr Leu Val Gly Lys Pro Leu Leu Ala Phe Arg Asn Leu Arg Pro Met
740 745 750

Leu Ala Ala Leu Ala Gln Arg Tyr Phe Thr Ala Ser Leu Pro Phe Glu
755 760 765

Lys Asn Cys Gly Ala Asp His Ile Cys Gln Asp Asn Leu Gly Ile Ser
770 775 780

Phe Ser Phe Pro Gly Leu Lys Ser Leu Leu Val Gly Ser Asn Leu Glu
785 790 795 800

Leu Asn Ala Glu Val Met Val Trp Asn Asp Gly Glu Asp Ser Tyr Gly
805 810 815

Thr Thr Ile Thr Phe Ser His Pro Ala Gly Leu Ser Tyr Arg Tyr Val
820 825 830

Ala Glu Gly Gln Lys Gln Gly Gln Leu Arg Ser Leu His Leu Thr Cys
835 840 845

Cys Ser Ala Pro Val Gly Ser Gln Gly Thr Trp Ser Thr Ser Cys Arg
850 855 860

Ile Asn His Leu Ile Phe Arg Gly Gly Ala Gln Ile Thr Phe Leu Ala
865 870 875 880

Thr Phe Asp Val Ser Pro Lys Ala Val Gly Leu Asp Arg Leu Leu Leu
885 890 895

Ile Ala Asn Val Ser Ser Glu Asn Asn Ile Pro Arg Thr Ser Lys Thr
900 905 910

Ile Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Ile Val Val
915 920 925

Ser Ser His Glu Gln Phe Thr Lys Tyr Leu Asn Phe Ser Glu Ser Glu
930 935 940

Glu Lys Glu Ser His Val Ala Met His Arg Tyr Gln Val Asn Asn Leu
945 950 955 960

Gly Gln Arg Asp Leu Pro Val Ser Ile Asn Phe Trp Val Pro Val Glu
965 970 975

Leu Asn Gln Glu Ala Val Trp Met Asp Val Glu Val Ser His Pro Gln
980 985 990

Asn Pro Ser Leu Arg Cys Ser Ser Glu Lys Ile Ala Pro Pro Ala Ser
995 1000 1005

Asp Phe Leu Ala His Ile Gln Lys Asn Pro Val Leu Asp Cys Ser Ile
1010 1015 1020

Ala Gly Cys Leu Arg Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln
1025 1030 1035 1040

Glu Glu Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val
1045 1050 1055

Arg Gln Ile Leu Gln Lys Lys Val Ser Val Val Ser Val Ala Glu Ile
1060 1065 1070

Ile Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe
1075 1080 1085

Met Arg Ala Gln Thr Ile Thr Val Leu Glu Lys Tyr Lys Val His Asn
1090 1095 1100

Pro Ile Pro Leu Ile Val Gly Ser Ser Ile Gly Gly Leu Leu Leu Leu
1105 1110 1115 1120

Ala Leu Ile Thr Ala Val Leu Tyr Lys Val Gly Phe Phe Lys Arg Gln
1125 1130 1135

Tyr Lys Glu Met Met Glu Glu Ala Asn Gly Gln Ile Ala Pro Glu Asn
1140 1145 1150

Gly Thr Gln Thr Pro Ser Pro Pro Ser Glu Lys
1155 1160

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Phe Asn Leu Asp Val Glu Glu Pro Met Val Phe Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTYAAYYTGG AYGTNGARGA RCCNATGGTN TTYCA 35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCAACCTGG ACGTGGAGGA GCCCATGGTG TTCCAA 36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCAACCTGG ACGTNGAASA NCCCATGGTC TTCCAA 36

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTYAAYYTNG AYGTNGARGA RCC 23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTYAAYYTGG ACGTNGAAGA 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGRAANACCA TNGGYTC 17

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTGGAAGACC ATNGGYTC 18

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATTAACCCTC ACTAAAG 17

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATACGACTC ACTATAG 17

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Phe Gln Glu Xaa Gly Ala Gly Phe Gly Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Tyr Asp Xaa Val Ala Ala Thr Gly Leu Xaa Gln Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Leu Glu Tyr Xaa Asp Val Ile Pro Gln Ala Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Gln Glu Gly Phe Ser Xaa Val Leu Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr Ser Pro Thr Phe Ile Xaa Met Ser Gln Glu Asn Val Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Val Val Gly Ala Pro Leu Glu Val Val Ala Val Xaa Gln Thr Gly
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Asp Xaa Lys Pro Xaa Asp Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Phe Gly Glu Gln Phe Ser Glu
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

RAANCCYTCY TGRAAACTYT C 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCAACCTGG ACGTGGAGGA GCCCATGGTG TTCAAGAGGA TGGAGCTGGC TTTGGACAGA 60

GCGTGGCCCA GCTTGGCGGA TCTAGACTCG TGGTGGGAGC CCCCCTGGAG GTGGTGGCGG 120

TCAACCAAAC AGGAAGGTTG TATGACTGTG TGGCTGCCAC TGGCCTTGTC AACCCATACC 180

CCTGCACACA CCCCCAGATG CTGTGAACAT GTCCCTGGGT CTGTCCCTGT CAGCCGCCGC 240

CAGTCGCCCC TGGCTGCTGG CCTGTGGCCC AACCATGCAC AGAGCCTGTG GGGAGAATAT 300

GTATGCAGAA GGCTTTTGCC TCCTGTTGGA CTCCCATCTG CAGACCATTT GGACAGTACC 360

TGCTGCCCTA CCAGAGTGTC CAAGTCAAGA GATGGACATT GTCTTCCTGA TTGATGGTTC 420

TGGCAGTATG AGCAAAGTGA CTTTAAACAA ATGAAGGATT TGTGAGAGCT GTGATGGGAC 480

AGTTTGAGGG CACCCAAACC CTGTTCTCAC TGATACAGTA TCCCACCTCC CTGAAGATCC 540

ACTTCACCTT CACGCAATTC CAGAGCAGCT GGAACCCTCT GAGCCTGGTG GATCCCATTG 600

TCCAACTGGA CGGCCTGACA TATACAGCCA CGGGCATCCG GAAAGTGGTG GAGGAACTGT 660

TTCATAGTAA GAATGGGGCC CGTAAAAGTG CCAAGAAGAT CCTCATTGTC ATCACAGATG 720

GCAAAAATAC AAAGACCCCC TGGAGTACGA GGACGTATCC CCAGGCAGAG AGAGCGGATC 780

ATCCGCTATG CCATTGGGGT GGGAGATGCT TTCTGGAAAC CCAGTGCCAA GCAGGAGCTG 840

GACAACATTG GCTCAGAGCC GGCTCAGGAC CATGTGTTCA GGGTGGACAA CTTTGCAGCA 900

CTCAGCAGCA TCCAGGAGCA GCTGCAGGAG AAGATCTTTG CACTCGAAGG AACCCAGTCG 960

ACGACAAGTA GCTCTTTCCA ACATGAGATG TTCCAAGAAG GGTTCA 1006

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTNTTYCARG ARGAYGG 17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCACTGTCAG GATGCCCGTG 20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGTTACGAAT TCGCCACCAT GGCTCTACGG GTGCTTCTTC TG 42

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGTTACGAAT TCGCCACCAT GACTCGGACT GTGCTTCTTC TG 42

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGTTACGAAT TCGCCACCAT GACCTTCGGC ACTGTG 36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGCTGACTG CCTGCAGTTC 20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTTCTGACGC GTAATGGCAT TGTAGACCTC GTCTTC 36

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACGTATGCAG GATCCCATCA AGAGATGGAC ATCGCT 36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACTGCATGTC TCGAGGCTGA AGCCTTCTTG GGACATC 37

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TATAGACTGC TGGGTAGTCC CCAC 24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGAAGATTGG GGGTAAATAA CAGA 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
GGC TGG GCC CTG GCT TCC TGT CAT GGG TCT AAC CTG GAT GTG GAG GAA      48
Gly Trp Ala Leu Ala Ser Cys His Gly Ser Asn Leu Asp Val Glu Glu
 1               5                  10                  15

CCC ATC GTG TTC AGA GAG GAT GCA GCC AGC TTT GGA CAG ACT GTG GTG      96
Pro Ile Val Phe Arg Glu Asp Ala Ala Ser Phe Gly Gln Thr Val Val
            20                  25                  30

CAG TTT GGT GGA TCT CGA CTC GTG GTG GGA GCC CCT CTG GAG GCG GTG     144
Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala Pro Leu Glu Ala Val
        35                  40                  45

GCA GTC AAC CAA ACA GGA CGG TTG TAT GAC TGT GCA CCT GCC ACT GGC     192
Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly
    50                  55                  60
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ATG TGC CAG CCC ATC GTA CTG CGC AGT CCC CTA GAG GCA GTG AAC ATG          240
Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu Glu Ala Val Asn Met
 65                  70                  75                  80

TCC CTG GGC CTG TCT CTG GTG ACT GCC ACC AAT AAC GCC CAG TTG CTG          288
Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn Asn Ala Gln Leu Leu
                 85                  90                  95

GCT TGT GGT CCA ACT GCA CAG AGA GCT TGT GTG AAG AAC ATG TAT GCG          336
Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val Lys Asn Met Tyr Ala
            100                 105                 110

AAA GGT TCC TGC CTC CTT CTC GGC TCC AGC TTG CAG TTC ATC CAG GCA          384
Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala
        115                 120                 125

GTC CCT GCC TCC ATG CCA GAG TGT CCA AGA CAA GAG ATG GAC ATT GCT          432
Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln Glu Met Asp Ile Ala
    130                 135                 140

TTC CTG ATT GAT GGT TCT GGC AGC ATT AAC CAA AGG GAC TTT GCC CAG          480
Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln
145                 150                 155                 160

ATG AAG GAC TTT GTC AAA GCT TTG ATG GGA GAG TTT GCG AGC ACC AGC          528
Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu Phe Ala Ser Thr Ser
                165                 170                 175

ACC TTG TTC TCC CTG ATG CAA TAC TCG AAC ATC CTG AAG ACC CAT TTT          576
Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile Leu Lys Thr His Phe
            180                 185                 190

ACC TTC ACT GAA TTC AAG AAC ATC CTG GAC CCT CAG AGC CTG GTG GAT          624
Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro Gln Ser Leu Val Asp
        195                 200                 205

CCC ATT GTC CAG CTG CAA GGC CTG ACC TAC ACA GCC ACA GGC ATC CGG          672
Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg
    210                 215                 220

ACA GTG ATG GAA GAG CTA TTT CAT AGC AAG AAT GGG TCC CGT AAA AGT          720
Thr Val Met Glu Glu Leu Phe His Ser Lys Asn Gly Ser Arg Lys Ser
225                 230                 235                 240

GCC AAG AAG ATC CTC CTT GTC ATC ACA GAT GGG CAG AAA TAC AGA GAC          768
Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp
                245                 250                 255

CCC CTG GAG TAT AGT GAT GTC ATT CCC GCC GCA GAC AAA GCT GGC ATC          816
Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala Asp Lys Ala Gly Ile
            260                 265                 270

ATT CGT TAT GCT ATT GGG GTG GGA GAT GCC TTC CAG GAG CCC ACT GCC          864
Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe Gln Glu Pro Thr Ala
        275                 280                 285

CTG AAG GAG CTG AAC ACC ATT GGC TCA GCT CCC CCA CAG GAC CAC GTG          912
Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro Pro Gln Asp His Val
    290                 295                 300
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TTC AAG GTA GGC AAC TTT GCA GCA CTT CGC AGC ATC CAG AGG CAA CTT        960
Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu
305                 310                 315                 320

CAG GAG AAA ATC TTC GCC ATT GAG GGA ACT CAA TCA AGG TCA AGT AGT       1008
Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser
                325                 330                 335

TCC TTT CAG CAC GAG ATG TCA CAA GAA GGT TTC AGT TCA GCT CTC ACA       1056
Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr
            340                 345                 350

TCG GAT GGA CCC GTT CTG GGG GCC GYG GGA AGC TTC AGC TGG TCC GGA       1104
Ser Asp Gly Pro Val Leu Gly Ala Xaa Gly Ser Phe Ser Trp Ser Gly
        355                 360                 365

GGT GCC TTC TTA TAT CCC CCA AAT ACG AGA CCC ACC TTT ATC AAC ATG       1152
Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro Thr Phe Ile Asn Met
    370                 375                 380

TCT CAG GAG AAT GTG GAC ATG AGA GAC TCC TAC CTG GGT TAC TCC ACC       1200
Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr
385                 390                 395                 400

GCA GTG GCC TTT TGG AAG GGG GTT CAC AGC CTG ATC CTG GGG GCC CCG       1248
Ala Val Ala Phe Trp Lys Gly Val His Ser Leu Ile Leu Gly Ala Pro
                405                 410                 415

CGT CAC CAG CAC ACG GGG AAG GTT GTC ATC TTT ACC CAG GAA GCC AGG       1296
Arg His Gln His Thr Gly Lys Val Val Ile Phe Thr Gln Glu Ala Arg
            420                 425                 430

CAT TGG AGG CCC AAG TCT GAA GTC AGA GGG ACA CAG ATC GGC TCC TAC       1344
His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr
        435                 440                 445

TTC GGG GCC TCT CTC TGT TCT GTG GAC GTG GAT AGA GAT GGC AGC ACY       1392
Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp Arg Asp Gly Ser Xaa
    450                 455                 460

GAC CTG GTC CTG ATC GGA GCC CCC CAT TAC TAT GAG CAG ACC CGA GGG       1440
Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly
465                 470                 475                 480

GGG CAG GTC TCA GTG TKC CCC GTG CCC GGT GTG AGG GGC AGG TGG CAG       1488
Gly Gln Val Ser Val Xaa Pro Val Pro Gly Val Arg Gly Arg Trp Gln
                485                 490                 495

TGT GAG GCC ACC CTC CAC GGG GAG CAG GRC CAT CCT TGG GGC CGC TTT       1536
Cys Glu Ala Thr Leu His Gly Glu Gln Xaa His Pro Trp Gly Arg Phe
            500                 505                 510

GGG GTG GCT CTG ACA GTG CTG GGG GAC GTA AAC GGG GAC AAT CTG GCA       1584
Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn Gly Asp Asn Leu Ala
        515                 520                 525

GAC GTG GCT ATT GGT GCC CCT GGA GAG GAG GAG AGC AGA GGT GCT GTC       1632
Asp Val Ala Ile Gly Ala Pro Gly Glu Glu Glu Ser Arg Gly Ala Val
    530                 535                 540
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TAC ATA TTT CAT GGA GCC TCG AGA CTG GAG ATC ATG CCC TCA CCC AGC      1680
Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile Met Pro Ser Pro Ser
545                 550                 555                 560

CAG CGG GTC ACT GGC TCC CAG CTC TCC CTG AGA CTG CAG TAT TTT GGG      1728
Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly
                565                 570                 575

CAG TCA TTG AGT GGG GGT CAG GAC CTT ACA CAG GAT GGC CTG GTG GAC      1776
Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln Asp Gly Leu Val Asp
            580                 585                 590

CTG GCC GTG GGA GCC CAG GGG CAC GTA CTG CTG CTC AGG AGT CTG CCT      1824
Leu Ala Val Gly Ala Gln Gly His Val Leu Leu Leu Arg Ser Leu Pro
        595                 600                 605

CTG CTG AAA GTG GAG CTC TCC ATA AGA TTC GCC CCC ATG GAG GTG GCA      1872
Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala Pro Met Glu Val Ala
    610                 615                 620

AAG GCT GTG TAC CAG TGC TGG GAA AGG ACT CCC ACT GTC CTC GAA GCT      1920
Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro Thr Val Leu Glu Ala
625                 630                 635                 640

GGA GAG GCC ACT GTC TGT CTC ACT GTC CAC AAA GGC TCA CCT GAC CTG      1968
Gly Glu Ala Thr Val Cys Leu Thr Val His Lys Gly Ser Pro Asp Leu
                645                 650                 655

TTA GGT AAT GTC CAA GGC TCT GTC AGG TAT GAT CTG GCG TTA GAT CCG      2016
Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro
            660                 665                 670

GGC CGC CTG ATT TCT CGT GCC ATT TTT GAT GAG ACT AAG AAC TGC ACT      2064
Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr
        675                 680                 685

TTG ACG GGA AGG AAG ACT CTG GGG CTT GGT GAT CAC TGC GAA ACA GTG      2112
Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp His Cys Glu Thr Val
    690                 695                 700

AAG CTG CTT TTG CCG GAC TGT GTG GAA GAT GCA GTG AGC CCT ATC ATC      2160
Lys Leu Leu Leu Pro Asp Cys Val Glu Asp Ala Val Ser Pro Ile Ile
705                 710                 715                 720

CTG CGC CTC AAC TTT TCC CTG GTG AGA GAC TCT GCT TCA CCC AGG AAC      2208
Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser Ala Ser Pro Arg Asn
                725                 730                 735

CTG CAT CCT GTG CTG GCT GTG GGC TCA CAA GAC CAC ATA ACT GCT TCT      2256
Leu His Pro Val Leu Ala Val Gly Ser Gln Asp His Ile Thr Ala Ser
            740                 745                 750

CTG CCG TTT GAG AAG AAC TGT AAG CAA GAA CTC CTG TGT GAG GGG GAC      2304
Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp
        755                 760                 765

CTG GGC ATC AGC TTT AAC TTC TCA GGC CTG CAG GTC TTG GTG GTG GGA      2352
Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Val Val Gly
    770                 775                 780
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GGC TCC CCA GAG CTC ACT GTG ACA GTC ACT GTG TGG AAT GAG GGT GAG          2400
Gly Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp Asn Glu Gly Glu
785                 790                 795                 800

GAC AGC TAT GGA ACT TTA GTC AAG TTC TAC TAC CCA GCA GGG CTA TCT          2448
Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser
                805                 810                 815

TAC CGA CGG GTA ACA GGG ACT CAG CAA CCT CAT CAG TAC CCA CTA CGC          2496
Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His Gln Tyr Pro Leu Arg
            820                 825                 830

TTG GCC TGT GAG GCT GAG CCC GCT GCC CAG GAG GAC CTG AGG AGC AGC          2544
Leu Ala Cys Glu Ala Glu Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser
        835                 840                 845

AGC TGT AGC ATT AAT CAC CCC ATC TTC CGA GAA GGT GCA AAG ACC ACC          2592
Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr
    850                 855                 860

TTC ATG ATC ACA TTC GAT GTC TCC TAC AAG GCC TTC CTA GGA GAC AGG          2640
Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg
865                 870                 875                 880

TTG CTT CTG AGG GCC AAA GCC AGC AGT GAG AAT AAT AAG CCT GAT ACC          2688
Leu Leu Leu Arg Ala Lys Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr
                885                 890                 895

AAC AAG ACT GCC TTC CAG CTG GAG CTC CCA GTG AAG TAC ACC GTC TAT          2736
Asn Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr
            900                 905                 910

ACC CTG ATC AGT AGG CAA GAA GAT TCC ACC AAC CAT GTC AAC TTT TCA          2784
Thr Leu Ile Ser Arg Gln Glu Asp Ser Thr Asn His Val Asn Phe Ser
        915                 920                 925

TCT TCC CAC GGG GGG AGA AGG CAA GAA GCC GCA CAT CGC TAT CGT GTG          2832
Ser Ser His Gly Gly Arg Arg Gln Glu Ala Ala His Arg Tyr Arg Val
    930                 935                 940

AAT AAC CTG AGT CCA CTG AAG CTG GCC GTC AGA GTT AAC TTC TGG GTC          2880
Asn Asn Leu Ser Pro Leu Lys Leu Ala Val Arg Val Asn Phe Trp Val
945                 950                 955                 960

CCT GTC CTT CTG AAC GGT GTG GCT GTG TGG GAC GTG ACT CTG AGC AGC          2928
Pro Val Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu Ser Ser
                965                 970                 975

CCA GCA CAG GGT GTC TCC TGC GTG TCC CAG ATG AAA CCT CCT CAG AAT          2976
Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met Lys Pro Pro Gln Asn
            980                 985                 990

CCC GAC TTT CTG ACC CAG ATT CAG AGA CGT TCT GTG CTG GAC TGC TCC          3024
Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser Val Leu Asp Cys Ser
        995                 1000                1005

ATT GCT GAC TGC CTG CAC TCC CGC TGT GAC ATC CCC TCC TTG GAC ATC          3072
Ile Ala Asp Cys Leu His Ser Arg Cys Asp Ile Pro Ser Leu Asp Ile
    1010                1015                1020
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CAG GAT GAA CTT GAC TTC ATT CTG AGG GGC AAC CTC AGC TTC GGC TGG       3120
Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp
1025                1030                1035                1040

GTC AGT CAG ACA TTG CAG GAA AAG GTG TTG CTT GTG AGT GAG GCT GAA       3168
Val Ser Gln Thr Leu Gln Glu Lys Val Leu Leu Val Ser Glu Ala Glu
                1045                1050                1055

ATC ACT TTC GAC ACA TCT GTG TAC TCC CAG CTG CCA GGA CAG GAG GCA       3216
Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala
            1060                1065                1070

TTT CTG AGA GCC CAG GTG GAG ACA ACG TTA GAA GAA TAC GTG GTC TAT       3264
Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu Glu Tyr Val Val Tyr
        1075                1080                1085

GAG CCC ATC TTC CTC GTG GCG GGC AGC TCG GTG GGA GGT CTG CTG TTA       3312
Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val Gly Gly Leu Leu Leu
    1090                1095                1100

CTG GCT CTC ATC ACA GTG GTA CTG TAC AAG CTT GGC TYC TYC AAA CGT       3360
Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu Gly Xaa Xaa Lys Arg
1105                1110                1115                1120

CAG TAC AAA GAA ATG CTG GAC GGC AAG GCT GCA GAT CCT GTC ACA GCC       3408
Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala Asp Pro Val Thr Ala
                1125                1130                1135

GGC CAG GCA GAT TTC GGC TGT GAG ACT CCT CCA TAT CTC GTG AGC TAGGAATCCA   3463
Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro Tyr Leu Val Ser
            1140                1145                1150

CTCTCCTGCC TATCTCTGNA ATGAAGATTG GTCCTGCCTA TGAGTCTACT GGCATGGGAA     3523

CGAGT                                                                 3528
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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1151 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Gly Trp Ala Leu Ala Ser Cys His Gly Ser Asn Leu Asp Val Glu Glu
  1               5                  10                  15

Pro Ile Val Phe Arg Glu Asp Ala Ala Ser Phe Gly Gln Thr Val Val
            20                  25                  30

Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala Pro Leu Glu Ala Val
        35                  40                  45

Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly
    50                  55                  60
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Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu Glu Ala Val Asn Met
65 70 75 80

Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn Asn Ala Gln Leu Leu
85 90 95

Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val Lys Asn Met Tyr Ala
100 105 110

Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala
115 120 125

Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln Glu Met Asp Ile Ala
130 135 140

Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln
145 150 155 160

Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu Phe Ala Ser Thr Ser
165 170 175

Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile Leu Lys Thr His Phe
180 185 190

Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro Gln Ser Leu Val Asp
195 200 205

Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg
210 215 220

Thr Val Met Glu Glu Leu Phe His Ser Lys Asn Gly Ser Arg Lys Ser
225 230 235 240

Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp
245 250 255

Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala Asp Lys Ala Gly Ile
260 265 270

Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe Gln Glu Pro Thr Ala
275 280 285

Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro Pro Gln Asp His Val
290 295 300

Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu
305 310 315 320

Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser
325 330 335

Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr
340 345 350

Ser Asp Gly Pro Val Leu Gly Ala Xaa Gly Ser Phe Ser Trp Ser Gly
355 360 365

Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro Thr Phe Ile Asn Met
370 375 380

Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr
385 390 395 400

Ala Val Ala Phe Trp Lys Gly Val His Ser Leu Ile Leu Gly Ala Pro
405 410 415

Arg His Gln His Thr Gly Lys Val Val Ile Phe Thr Gln Glu Ala Arg
420 425 430

His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr
435 440 445

Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp Arg Asp Gly Ser Xaa
450 455 460

Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly
465 470 475 480

Gly Gln Val Ser Val Xaa Pro Val Pro Gly Val Arg Gly Arg Trp Gln
485 490 495

Cys Glu Ala Thr Leu His Gly Glu Gln Xaa His Pro Trp Gly Arg Phe
500 505 510

Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn Gly Asp Asn Leu Ala
515 520 525

Asp Val Ala Ile Gly Ala Pro Gly Glu Glu Glu Ser Arg Gly Ala Val
530 535 540

Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile Met Pro Ser Pro Ser
545 550 555 560

Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly
565 570 575

Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln Asp Gly Leu Val Asp
580 585 590

Leu Ala Val Gly Ala Gln Gly His Val Leu Leu Leu Arg Ser Leu Pro
595 600 605

Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala Pro Met Glu Val Ala
610 615 620

Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro Thr Val Leu Glu Ala
625 630 635 640

Gly Glu Ala Thr Val Cys Leu Thr Val His Lys Gly Ser Pro Asp Leu
645 650 655

Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro
660 665 670

Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr
675 680 685

Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp His Cys Glu Thr Val
690 695 700

Lys Leu Leu Leu Pro Asp Cys Val Glu Asp Ala Val Ser Pro Ile Ile
705 710 715 720

Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser Ala Ser Pro Arg Asn
725 730 735

Leu His Pro Val Leu Ala Val Gly Ser Gln Asp His Ile Thr Ala Ser
740 745 750

Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp
755 760 765

Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Val Val Gly
770 775 780

Gly Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp Asn Glu Gly Glu
785 790 795 800

Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser
805 810 815

Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His Gln Tyr Pro Leu Arg
820 825 830

Leu Ala Cys Glu Ala Glu Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser
835 840 845

Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr
850 855 860

Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg
865 870 875 880

Leu Leu Leu Arg Ala Lys Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr
885 890 895

Asn Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr
900 905 910

Thr Leu Ile Ser Arg Gln Glu Asp Ser Thr Asn His Val Asn Phe Ser
915 920 925

Ser Ser His Gly Gly Arg Arg Gln Glu Ala Ala His Arg Tyr Arg Val
930 935 940

Asn Asn Leu Ser Pro Leu Lys Leu Ala Val Arg Val Asn Phe Trp Val
945 950 955 960

Pro Val Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu Ser Ser
965 970 975

Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met Lys Pro Pro Gln Asn
980 985 990

Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser Val Leu Asp Cys Ser
995 1000 1005

Ile Ala Asp Cys Leu His Ser Arg Cys Asp Ile Pro Ser Leu Asp Ile
1010 1015 1020

Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp
1025 1030 1035 1040

Val Ser Gln Thr Leu Gln Glu Lys Val Leu Leu Val Ser Glu Ala Glu
1045 1050 1055

Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala
1060 1065 1070

Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu Glu Tyr Val Val Tyr
1075 1080 1085

Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val Gly Gly Leu Leu Leu
1090 1095 1100

Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu Gly Xaa Xaa Lys Arg
1105 1110 1115 1120

Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala Asp Pro Val Thr Ala
1125 1130 1135

Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro Tyr Leu Val Ser
1140 1145 1150

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCCAAGCTG TCATGGGCCA G 21

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTCCAGCAGA CTGAAGAGCA CGG 23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGTAAAACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGAAACAGCT ATGACCATG 19

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGACATGTTC ACTGCCTCTA GG 22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCGGACAGT CAGACGACTG TCCTG 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 52..3519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

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GCTTTCTGAA GGTTCCAGAA TCGATAGTGA ATTCGTGGGC ACTGCTCAGA T ATG GTC      57
                                                          Met Val
                                                            1

CGT GGA GTT GTG ATC CTC CTG TGT GGC TGG GCC CTG GCT TCC TGT CAT      105
Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser Cys His
          5                  10                  15

GGG TCT AAC CTG GAT GTG GAG AAG CCC GTC GTG TTC AAA GAG GAT GCA      153
Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu Asp Ala
      20                  25                  30

GCC AGC TTC GGA CAG ACT GTG GTG CAG TTT GGT GGA TCT CGA CTC GTG      201
Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg Leu Val
  35                  40                  45                  50

GTG GGA GCC CCT CTG GAG GCG GTG GCA GTC AAC CAA ACA GGA CAG TCG      249
Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly Gln Ser
                  55                  60                  65

TCT GAC TGT CCG CCT GCC ACT GGC GTG TGC CAG CCC ATC TTA CTG CAC      297
Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu Leu His
              70                  75                  80

ATT CCC CTA GAG GCA GTG AAC ATG TCC CTG GGC CTG TCT CTG GTG GCT      345
Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Val Ala
          85                  90                  95
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GAC ACC AAT AAC TCC CAG TTG CTG GCT TGT GGT CCA ACT GCA CAG AGA          393
Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala Gln Arg
    100                 105                 110

GCT TGT GCA AAG AAC ATG TAT GCA AAA GGT TCC TGC CTC CTT CTG GGC          441
Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu Leu Gly
115                 120                 125                 130

TCC AGC TTG CAG TTC ATC CAG GCA ATC CCT GCT ACC ATG CCA GAG TGT          489
Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro Glu Cys
                135                 140                 145

CCA GGA CAA GAG ATG GAC ATT GCT TTC CTG ATT GAT GGC TCC GGC AGC          537
Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
            150                 155                 160

ATT GAT CAA AGT GAC TTT ACC CAG ATG AAG GAC TTC GTC AAA GCT TTG          585
Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys Ala Leu
        165                 170                 175

ATG GGC CAG TTG GCG AGC ACC AGC ACC TCG TTC TCC CTG ATG CAA TAC          633
Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met Gln Tyr
    180                 185                 190

TCA AAC ATC CTG AAG ACT CAT TTT ACC TTC ACG GAA TTC AAG AGC AGC          681
Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys Ser Ser
195                 200                 205                 210

CTG AGC CCT CAG AGC CTG GTG GAT GCC ATC GTC CAG CTC CAA GGC CTG          729
Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln Gly Leu
                215                 220                 225

ACG TAC ACA GCC TCG GGC ATC CAG AAA GTG GTG AAA GAG CTA TTT CAT          777
Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu Phe His
            230                 235                 240

AGC AAG AAT GGG GCC CGA AAA AGT GCC AAG AAG ATA CTA ATT GTC ATC          825
Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile Val Ile
        245                 250                 255

ACA GAT GGG CAG AAA TTC AGA GAC CCC CTG GAG TAT AGA CAT GTC ATC          873
Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His Val Ile
    260                 265                 270

CCT GAA GCA GAG AAA GCT GGG ATC ATT CGC TAT GCT ATA GGG GTG GGA          921
Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly
275                 280                 285                 290

GAT GCC TTC CGG GAA CCC ACT GCC CTA CAG GAG CTG AAC ACC ATT GGC          969
Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr Ile Gly
                295                 300                 305

TCA GCT CCC TCG CAG GAC CAC GTG TTC AAG GTG GGC AAT TTT GTA GCA         1017
Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe Val Ala
            310                 315                 320

CTT CGC AGC ATC CAG CGG CAA ATT CAG GAG AAA ATC TTT GCC ATT GAA         1065
Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala Ile Glu
        325                 330                 335
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GGA ACC GAA TCA AGG TCA AGT AGT TCC TTT CAG CAC GAG ATG TCA CAA      1113
Gly Thr Glu Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met Ser Gln
    340                 345                 350

GAA GGT TTC AGC TCA GCT CTC TCA ATG GAT GGA CCA GTT CTG GGG GCT      1161
Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu Gly Ala
355                 360                 365                 370

GTG GGA GGC TTC AGC TGG TCT GGA GGT GCC TTC TTG TAC CCC TCA AAT      1209
Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Ser Asn
                375                 380                 385

ATG AGA TCC ACC TTC ATC AAC ATG TCT CAG GAG AAC GAG GAT ATG AGG      1257
Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp Met Arg
            390                 395                 400

GAC GCT TAC CTG GGT TAC TCC ACC GCA CTG GCC TTT TGG AAG GGG GTC      1305
Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys Gly Val
        405                 410                 415

CAC AGC CTG ATC CTG GGG GCC CCT CGC CAC CAG CAC ACG GGG AAG GTT      1353
His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly Lys Val
    420                 425                 430

GTC ATC TTT ACC CAG GAA TCC AGG CAC TGG AGG CCC AAG TCT GAA GTC      1401
Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser Glu Val
435                 440                 445                 450

AGA GGG ACA CAG ATC GGC TCC TAC TTT GGG GCA TCT CTC TGT TCT GTG      1449
Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val
                455                 460                 465

GAC ATG GAT AGA GAT GGC AGC ACT GAC CTG GTC CTG ATT GGA GTC CCC      1497
Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly Val Pro
            470                 475                 480

CAT TAC TAT GAG CAC ACC CGA GGG GGG CAG GTG TCG GTG TGC CCC ATG      1545
His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys Pro Met
        485                 490                 495

CCT GGT GTG AGG AGC AGG TGG CAT TGT GGG ACC ACC CTC CAT GGG GAG      1593
Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His Gly Glu
    500                 505                 510

CAG GGC CAT CCT TGG GGC CGC TTT GGG GCG GCT CTG ACA GTG CTA GGG      1641
Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu Gly
515                 520                 525                 530

GAC GTG AAT GGG GAC AGT CTG GCG GAT GTG GCT ATT GGT GCA CCC GGA      1689
Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala Pro Gly
                535                 540                 545

GAG GAG GAG AAC AGA GGT GCT GTC TAC ATA TTT CAT GGA GCC TCG AGA      1737
Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala Ser Arg
            550                 555                 560

CAG GAC ATC GCT CCC TCG CCT AGC CAG CGG GTC ACT GGC TCC CAG CTC      1785
Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser Gln Leu
        565                 570                 575
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TTC CTG AGG CTC CAA TAT TTT GGG CAG TCA TTA AGT GGG GGT CAG GAC          1833
Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln Asp
    580                 585                 590

CTT ACA CAG GAT GGC CTG GTG GAC CTG GCC GTG GGA GCC CAG GGG CAC          1881
Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln Gly His
595                 600                 605                 610

GTG CTG CTG CTT AGG AGT CTG CCT TTG CTG AAA GTG GGG ATC TCC ATT          1929
Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile Ser Ile
                615                 620                 625

AGA TTT GCC CCC TCA GAG GTG GCA AAG ACT GTG TAC CAG TGC TGG GGA          1977
Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys Trp Gly
            630                 635                 640

AGG ACT CCC ACT GTC CTC GAA GCT GGA GAG GCC ACC GTC TGT CTC ACT          2025
Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys Leu Thr
        645                 650                 655

GTC CGC AAA GGT TCA CCT GAC CTG TTA GGT GAT GTC CAA AGC TCT GTC          2073
Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser Ser Val
    660                 665                 670

AGG TAT GAT CTG GCG TTG GAT CCG GGC CGT CTG ATT TCT CGT GCC ATT          2121
Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg Ala Ile
675                 680                 685                 690

TTT GAT GAG ACG AAG AAC TGC ACT TTG ACC CGA AGG AAG ACT CTG GGG          2169
Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr Leu Gly
                695                 700                 705

CTT GGT GAT CAC TGC GAA ACA ATG AAG CTG CTT TTG CCA GAC TGT GTG          2217
Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp Cys Val
            710                 715                 720

GAG GAT GCA GTG ACC CCT ATC ATC CTG CGC CTT AAC TTA TCC CTG GCA          2265
Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser Leu Ala
        725                 730                 735

GGG GAC TCT GCT CCA TCC AGG AAC CTT CGT CCT GTG CTG GCT GTG GGC          2313
Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala Val Gly
    740                 745                 750

TCA CAA GAC CAT GTA ACA GCT TCT TTC CCG TTT GAG AAG AAC TGT GAG          2361
Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn Cys Glu
755                 760                 765                 770

GGG AAC CTG GGC GTC AGC TTC AAC TTC TCA GGC CTG CAG GTC TTG GAG          2409
Gly Asn Leu Gly Val Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Glu
                775                 780                 785

GTA GGA AGC TCC CCA GAG CTC ACT GTG ACA GTA ACA GTT TGG AAT GAG          2457
Val Gly Ser Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp Asn Glu
            790                 795                 800

GGT GAG GAC AGC TAT GGA ACC TTA ATC AAG TTC TAC TAC CCA GCA GAG          2505
Gly Glu Asp Ser Tyr Gly Thr Leu Ile Lys Phe Tyr Tyr Pro Ala Glu
        805                 810                 815
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CTA TCT TAC CGA CGG GTG ACA AGA GCC CAG CAA CCT CAT CCG TAC CCA      2553
Leu Ser Tyr Arg Arg Val Thr Arg Ala Gln Gln Pro His Pro Tyr Pro
     820                 825                 830

CTA CGC CTG GCA TGT GAG GCT GAG CCC ACG GGC CAG GAG AGC CTG AGG      2601
Leu Arg Leu Ala Cys Glu Ala Glu Pro Thr Gly Gln Glu Ser Leu Arg
835                 840                 845                 850

AGC AGC AGC TGT AGC ATC AAT CAC CCC ATC TTC CGA GAA GGT GCC AAG      2649
Ser Ser Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys
                855                 860                 865

GCC ACC TTC ATG ATC ACA TTT GAT GTC TCC TAC AAG GCC TTC CTG GGA      2697
Ala Thr Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly
            870                 875                 880

GAC AGG TTG CTT CTG AGG GCC AGC GCA AGC AGT GAG AAT AAT AAG CCT      2745
Asp Arg Leu Leu Leu Arg Ala Ser Ala Ser Ser Glu Asn Asn Lys Pro
        885                 890                 895

GAA ACC AGC AAG ACT GCC TTC CAG CTG GAG CTT CCG GTG AAG TAC ACG      2793
Glu Thr Ser Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr
    900                 905                 910

GTC TAT ACC GTG ATC AGT AGG CAG GAA GAT TCT ACC AAG CAT TTC AAC      2841
Val Tyr Thr Val Ile Ser Arg Gln Glu Asp Ser Thr Lys His Phe Asn
915                 920                 925                 930

TTC TCA TCT TCC CAC GGG GAG AGA CAG AAA GAG GCC GAA CAT CGA TAT      2889
Phe Ser Ser Ser His Gly Glu Arg Gln Lys Glu Ala Glu His Arg Tyr
                935                 940                 945

CGT GTG AAT AAC CTG AGT CCA TTG ACG CTG GCC ATC AGC GTT AAC TTC      2937
Arg Val Asn Asn Leu Ser Pro Leu Thr Leu Ala Ile Ser Val Asn Phe
            950                 955                 960

TGG GTC CCC ATC CTT CTG AAT GGT GTG GCC GTG TGG GAT GTG ACT CTG      2985
Trp Val Pro Ile Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu
        965                 970                 975

AGG AGC CCA GCA CAG GGT GTC TCC TGT GTG TCA CAG AGG GAA CCT CCT      3033
Arg Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Arg Glu Pro Pro
    980                 985                 990

CAA CAT TCC GAC CTT CTG ACC CAG ATC CAA GGA CGC TCT GTG CTG GAC      3081
Gln His Ser Asp Leu Leu Thr Gln Ile Gln Gly Arg Ser Val Leu Asp
995                 1000                1005                1010

TGC GCC ATC GCC GAC TGC CTG CAC CTC CGC TGT GAC ATC CCC TCC TTG      3129
Cys Ala Ile Ala Asp Cys Leu His Leu Arg Cys Asp Ile Pro Ser Leu
                1015                1020                1025

GGC ACC CTG GAT GAG CTT GAC TTC ATT CTG AAG GGC AAC CTC AGC TTC      3177
Gly Thr Leu Asp Glu Leu Asp Phe Ile Leu Lys Gly Asn Leu Ser Phe
            1030                1035                1040

GGC TGG ATC AGT CAG ACA TTG CAG AAA AAG GTG TTG CTC CTG AGT GAG      3225
Gly Trp Ile Ser Gln Thr Leu Gln Lys Lys Val Leu Leu Leu Ser Glu
        1045                1050                1055
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GCT GAA ATC ACA TTC AAC ACA TCT GTG TAT TCC CAG CTG CCG GGA CAG      3273
Ala Glu Ile Thr Phe Asn Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln
    1060                1065                1070

GAG GCA TTT CTG AGA GCC CAG GTG TCA ACG ATG CTA GAA GAA TAC GTG      3321
Glu Ala Phe Leu Arg Ala Gln Val Ser Thr Met Leu Glu Glu Tyr Val
1075                1080                1085                1090

GTC TAT GAG CCC GTC TTC CTC ATG GTG TTC AGC TCA GTG GGA GGT CTG      3369
Val Tyr Glu Pro Val Phe Leu Met Val Phe Ser Ser Val Gly Gly Leu
                1095                1100                1105

CTG TTA CTG GCT CTC ATC ACT GTG GCG CTG TAC AAG CTT GGC TTC TTC      3417
Leu Leu Leu Ala Leu Ile Thr Val Ala Leu Tyr Lys Leu Gly Phe Phe
            1110                1115                1120

AAA CGT CAG TAT AAA GAG ATG CTG GAT CTA CCA TCT GCA GAT CCT GAC      3465
Lys Arg Gln Tyr Lys Glu Met Leu Asp Leu Pro Ser Ala Asp Pro Asp
        1125                1130                1135

CCA GCC GGC CAG GCA GAT TCC AAC CAT GAG ACT CCT CCA CAT CTC ACG      3513
Pro Ala Gly Gln Ala Asp Ser Asn His Glu Thr Pro Pro His Leu Thr
    1140                1145                1150

TCC TAG                                                             3519
Ser
1155
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Met Val Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser
  1               5                  10                  15

Cys His Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu
            20                  25                  30

Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg
        35                  40                  45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
    50                  55                  60

Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu
65                  70                  75                  80

Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
                85                  90                  95

Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala
            100                 105                 110
```

Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
115 120 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro
130 135 140

Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145 150 155 160

Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys
165 170 175

Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met
180 185 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
195 200 205

Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln
210 215 220

Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu
225 230 235 240

Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile
245 250 255

Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His
260 265 270

Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
275 280 285

Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp
385 390 395 400

Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly
465 470 475 480

Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys
485 490 495

Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
610 615 620

Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625 630 635 640

Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
725 730 735

Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
740 745 750

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Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
        755                 760                 765

Cys Glu Gly Asn Leu Gly Val Ser Phe Asn Phe Ser Gly Leu Gln Val
    770                 775                 780

Leu Glu Val Gly Ser Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp
785                 790                 795                 800

Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu Ile Lys Phe Tyr Tyr Pro
                805                 810                 815

Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg Ala Gln Gln Pro His Pro
            820                 825                 830

Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu Pro Thr Gly Gln Glu Ser
        835                 840                 845

Leu Arg Ser Ser Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly
    850                 855                 860

Ala Lys Ala Thr Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe
865                 870                 875                 880

Leu Gly Asp Arg Leu Leu Leu Arg Ala Ser Ala Ser Ser Glu Asn Asn
                885                 890                 895

Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys
            900                 905                 910

Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln Glu Asp Ser Thr Lys His
        915                 920                 925

Phe Asn Phe Ser Ser Ser His Gly Glu Arg Gln Lys Glu Ala Glu His
    930                 935                 940

Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu Thr Leu Ala Ile Ser Val
945                 950                 955                 960

Asn Phe Trp Val Pro Ile Leu Leu Asn Gly Val Ala Val Trp Asp Val
                965                 970                 975

Thr Leu Arg Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Arg Glu
            980                 985                 990

Pro Pro Gln His Ser Asp Leu Leu Thr Gln Ile Gln Gly Arg Ser Val
        995                 1000                1005

Leu Asp Cys Ala Ile Ala Asp Cys Leu His Leu Arg Cys Asp Ile Pro
    1010                1015                1020

Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe Ile Leu Lys Gly Asn Leu
1025                1030                1035                1040

Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln Lys Lys Val Leu Leu Leu
                1045                1050                1055

Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser Val Tyr Ser Gln Leu Pro
            1060                1065                1070
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Gly Gln Glu Ala Phe Leu Arg Ala Gln Val Ser Thr Met Leu Glu Glu
1075 1080 1085

Tyr Val Val Tyr Glu Pro Val Phe Leu Met Val Phe Ser Ser Val Gly
1090 1095 1100

Gly Leu Leu Leu Leu Ala Leu Ile Thr Val Ala Leu Tyr Lys Leu Gly
1105 1110 1115 1120

Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu Asp Leu Pro Ser Ala Asp
1125 1130 1135

Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn His Glu Thr Pro Pro His
1140 1145 1150

Leu Thr Ser
1155

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGTTACGGAT CCGGCACCAT GACCTTCGGC ACTGTGATCC TCCTGTGTG 49

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCTGGACGAT GGCATCCAC 19

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTAGAGTTAC GGATCCGGCA CCAT 24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGCCAGCT TCGGACAGAC 20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCATGTCCAC AGAACAGAGA G 21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
ATG GTC CGT GGA GTT GTG ATC CTC CTG TGT GGC TGG GCC CTG GCT TCC      48
Met Val Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser
 1               5                  10                  15

TGT CAT GGG TCT AAC CTG GAT GTG GAG AAG CCC GTC GTG TTC AAA GAG      96
Cys His Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu
            20                  25                  30
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GAT GCA GCC AGC TTC GGA CAG ACT GTG GTG CAG TTT GGT GGA TCT CGA        144
Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg
          35                  40                  45

CTC GTG GTG GGA GCC CCT CTG GAG GCG GTG GCA GTC AAC CAA ACA GGA        192
Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
      50                  55                  60

CAG TCG TCT GAC TGT CCG CCT GCC ACT GGC GTG TGC CAG CCC ATC TTA        240
Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu
 65                  70                  75                  80

CTG CAC ATT CCC CTA GAG GCA GTG AAC ATG TCC CTG GGC CTG TCT CTG        288
Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
                 85                  90                  95

GTG GCT GAC ACC AAT AAC TCC CAG TTG CTG GCT TGT GGT CCA ACT GCA        336
Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala
            100                 105                 110

CAG AGA GCT TGT GCA AAG AAC ATG TAT GCA AAA GGT TCC TGC CTC CTT        384
Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
        115                 120                 125

CTG GGC TCC AGC TTG CAG TTC ATC CAG GCA ATC CCT GCT ACC ATG CCA        432
Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro
    130                 135                 140

GAG TGT CCA GGA CAA GAG ATG GAC ATT GCT TTC CTG ATT GAT GGC TCC        480
Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145                 150                 155                 160

GGC AGC ATT GAT CAA AGT GAC TTT ACC CAG ATG AAG GAC TTC GTC AAA        528
Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys
                165                 170                 175

GCT TTG ATG GGC CAG TTG GCG AGC ACC AGC ACC TCG TTC TCC CTG ATG        576
Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met
            180                 185                 190

CAA TAC TCA AAC ATC CTG AAG ACT CAT TTT ACC TTC ACG GAA TTC AAG        624
Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
        195                 200                 205

AGC AGC CTG AGC CCT CAG AGC CTG GTG GAT GCC ATC GTC CAG CTC CAA        672
Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln
    210                 215                 220

GGC CTG ACG TAC ACA GCC TCG GGC ATC CAG AAA GTG GTG AAA GAG CTA        720
Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu
225                 230                 235                 240

TTT CAT AGC AAG AAT GGG GCC CGA AAA AGT GCC AAG AAG ATA CTA ATT        768
Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile
                245                 250                 255

GTC ATC ACA GAT GGG CAG AAA TTC AGA GAC CCC CTG GAG TAT AGA CAT        816
Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His
            260                 265                 270
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GTC ATC CCT GAA GCA GAG AAA GCT GGG ATC ATT CGC TAT GCT ATA GGG          864
Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
        275                 280                 285

GTG GGA GAT GCC TTC CGG GAA CCC ACT GCC CTA CAG GAG CTG AAC ACC          912
Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr
    290                 295                 300

ATT GGC TCA GCT CCC TCG CAG GAC CAC GTG TTC AAG GTG GGC AAT TTT          960
Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe
305                 310                 315                 320

GTA GCA CTT CGC AGC ATC CAG CGG CAA ATT CAG GAG AAA ATC TTT GCC         1008
Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala
                325                 330                 335

ATT GAA GGA ACC GAA TCA AGG TCA AGT AGT TCC TTT CAG CAC GAG ATG         1056
Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met
            340                 345                 350

TCA CAA GAA GGT TTC AGC TCA GCT CTC TCA ATG GAT GGA CCA GTT CTG         1104
Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu
        355                 360                 365

GGG GCT GTG GGA GGC TTC AGC TGG TCT GGA GGT GCC TTC TTG TAC CCC         1152
Gly Ala Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
    370                 375                 380

TCA AAT ATG AGA TCC ACC TTC ATC AAC ATG TCT CAG GAG AAC GAG GAT         1200
Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp
385                 390                 395                 400

ATG AGG GAC GCT TAC CTG GGT TAC TCC ACC GCA CTG GCC TTT TGG AAG         1248
Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys
                405                 410                 415

GGG GTC CAC AGC CTG ATC CTG GGG GCC CCT CGC CAC CAG CAC ACG GGG         1296
Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
            420                 425                 430

AAG GTT GTC ATC TTT ACC CAG GAA TCC AGG CAC TGG AGG CCC AAG TCT         1344
Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser
        435                 440                 445

GAA GTC AGA GGG ACA CAG ATC GGC TCC TAC TTT GGG GCA TCT CTC TGT         1392
Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
    450                 455                 460

TCT GTG GAC ATG GAT AGA GAT GGC AGC ACT GAC CTG GTC CTG ATT GGA         1440
Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly
465                 470                 475                 480

GTC CCC CAT TAC TAT GAG CAC ACC CGA GGG GGG CAG GTG TCG GTG TGC         1488
Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys
                485                 490                 495

CCC ATG CCT GGT GTG AGG AGC AGG TGG CAT TGT GGG ACC ACC CTC CAT         1536
Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His
            500                 505                 510
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GGG GAG CAG GGC CAT CCT TGG GGC CGC TTT GGG GCG GCT CTG ACA GTG        1584
Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
        515                 520                 525

CTA GGG GAC GTG AAT GGG GAC AGT CTG GCG GAT GTG GCT ATT GGT GCA        1632
Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
    530                 535                 540

CCC GGA GAG GAG GAG AAC AGA GGT GCT GTC TAC ATA TTT CAT GGA GCC        1680
Pro Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545                 550                 555                 560

TCG AGA CAG GAC ATC GCT CCC TCG CCT AGC CAG CGG GTC ACT GGC TCC        1728
Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
                565                 570                 575

CAG CTC TTC CTG AGG CTC CAA TAT TTT GGG CAG TCA TTA AGT GGG GGT        1776
Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
            580                 585                 590

CAG GAC CTT ACA CAG GAT GGC CTG GTG GAC CTG GCC GTG GGA GCC CAG        1824
Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
        595                 600                 605

GGG CAC GTG CTG CTG CTT AGG AGT CTG CCT TTG CTG AAA GTG GGG ATC        1872
Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
    610                 615                 620

TCC ATT AGA TTT GCC CCC TCA GAG GTG GCA AAG ACT GTG TAC CAG TGC        1920
Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625                 630                 635                 640

TGG GGA AGG ACT CCC ACT GTC CTC GAA GCT GGA GAG GCC ACC GTC TGT        1968
Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
                645                 650                 655

CTC ACT GTC CGC AAA GGT TCA CCT GAC CTG TTA GGT GAT GTC CAA AGC        2016
Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
            660                 665                 670

TCT GTC AGG TAT GAT CTG GCG TTG GAT CCG GGC CGT CTG ATT TCT CGT        2064
Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
        675                 680                 685

GCC ATT TTT GAT GAG ACG AAG AAC TGC ACT TTG ACC CGA AGG AAG ACT        2112
Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr
    690                 695                 700

CTG GGG CTT GGT GAT CAC TGC GAA ACA ATG AAG CTG CTT TTG CCA GAC        2160
Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705                 710                 715                 720

TGT GTG GAG GAT GCA GTG ACC CCT ATC ATC CTG CGC CTT AAC TTA TCC        2208
Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
                725                 730                 735

CTG GCA GGG GAC TCT GCT CCA TCC AGG AAC CTT CGT CCT GTG CTG GCT        2256
Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
            740                 745                 750
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GTG GGC TCA CAA GAC CAT GTA ACA GCT TCT TTC CCG TTT GAG AAG AAC      2304
Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
        755                 760                 765

TGT AAG CAG GAG CTC CTG TGT GAG GGG AAC CTG GGC GTC AGC TTC AAC      2352
Cys Lys Gln Glu Leu Leu Cys Glu Gly Asn Leu Gly Val Ser Phe Asn
    770                 775                 780

TTC TCA GGC CTG CAG GTC TTG GAG GTA GGA AGC TCC CCA GAG CTC ACT      2400
Phe Ser Gly Leu Gln Val Leu Glu Val Gly Ser Ser Pro Glu Leu Thr
785                 790                 795                 800

GTG ACA GTA ACA GTT TGG AAT GAG GGT GAG GAC AGC TAT GGA ACC TTA      2448
Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
                805                 810                 815

ATC AAG TTC TAC TAC CCA GCA GAG CTA TCT TAC CGA CGG GTG ACA AGA      2496
Ile Lys Phe Tyr Tyr Pro Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg
            820                 825                 830

GCC CAG CAA CCT CAT CCG TAC CCA CTA CGC CTG GCA TGT GAG GCT GAG      2544
Ala Gln Gln Pro His Pro Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
        835                 840                 845

CCC ACG GGC CAG GAG AGC CTG AGG AGC AGC AGC TGT AGC ATC AAT CAC      2592
Pro Thr Gly Gln Glu Ser Leu Arg Ser Ser Ser Cys Ser Ile Asn His
    850                 855                 860

CCC ATC TTC CGA GAA GGT GCC AAG GCC ACC TTC ATG ATC ACA TTT GAT      2640
Pro Ile Phe Arg Glu Gly Ala Lys Ala Thr Phe Met Ile Thr Phe Asp
865                 870                 875                 880

GTC TCC TAC AAG GCC TTC CTG GGA GAC AGG TTG CTT CTG AGG GCC AGC      2688
Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Ser
                885                 890                 895

GCA AGC AGT GAG AAT AAT AAG CCT GAA ACC AGC AAG ACT GCC TTC CAG      2736
Ala Ser Ser Glu Asn Asn Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln
            900                 905                 910

CTG GAG CTT CCG GTG AAG TAC ACG GTC TAT ACC GTG ATC AGT AGG CAG      2784
Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln
        915                 920                 925

GAA GAT TCT ACC AAG CAT TTC AAC TTC TCA TCT TCC CAC GGG GAG AGA      2832
Glu Asp Ser Thr Lys His Phe Asn Phe Ser Ser Ser His Gly Glu Arg
    930                 935                 940

CAG AAA GAG GCC GAA CAT CGA TAT CGT GTG AAT AAC CTG AGT CCA TTG      2880
Gln Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945                 950                 955                 960

ACG CTG GCC ATC AGC GTT AAC TTC TGG GTC CCC ATC CTT CTG AAT GGT      2928
Thr Leu Ala Ile Ser Val Asn Phe Trp Val Pro Ile Leu Leu Asn Gly
                965                 970                 975

TTG GCC GTG TGG GAT GTG ACT CTG AGG AGC CCA GCA CAG GGT GTC TCC      2976
Leu Ala Val Trp Asp Val Thr Leu Arg Ser Pro Ala Gln Gly Val Ser
            980                 985                 990
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TGT GTG TCA CAG AGG GAA CCT CCT CAA CAT TCC GAC CTT CTG ACC CAG      3024
Cys Val Ser Gln Arg Glu Pro Pro Gln His Ser Asp Leu Leu Thr Gln
        995                 1000                1005

ATC CAA GGA CGC TCT GTG CTG GAC TGC GCC ATC GCC GAC TGC CTG CAC      3072
Ile Gln Gly Arg Ser Val Leu Asp Cys Ala Ile Ala Asp Cys Leu His
    1010                1015                1020

CTC CGC TGT GAC ATC CCC TCC TTG GGC ACC CTG GAT GAG CTT GAC TTC      3120
Leu Arg Cys Asp Ile Pro Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe
1025                1030                1035                1040

ATT CTG AAG GGC AAC CTC AGC TTC GGC TGG ATC AGT CAG ACA TTG CAG      3168
Ile Leu Lys Gly Asn Leu Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln
                1045                1050                1055

AAA AAG GTG TTG CTC CTG AGT GAG GCT GAA ATC ACA TTC AAC ACA TCT      3216
Lys Lys Val Leu Leu Leu Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser
            1060                1065                1070

GTG TAT TCC CAG CTG CCG GGA CAG GAG GCA TTT CTG AGA GCC CAG GTG      3264
Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
        1075                1080                1085

TCA ACG ATG CTA GAA GAA TAC GTG GTC TAT GAG CCC GTC TTC CTC ATG      3312
Ser Thr Met Leu Glu Glu Tyr Val Val Tyr Glu Pro Val Phe Leu Met
    1090                1095                1100

GTG TTC AGC TCA GTG GGA GGT CTG CTG TTA CTG GCT CTC ATC ACT GTG      3360
Val Phe Ser Ser Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Val
1105                1110                1115                1120

GCG CTG TAC AAG CTT GGC TTC TTC AAA CGT CAG TAT AAA GAG ATG CTG      3408
Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu
                1125                1130                1135

GAT CTA CCA TCT GCA GAT CCT GAC CCA GCC GGC CAG GCA GAT TCC AAC      3456
Asp Leu Pro Ser Ala Asp Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn
            1140                1145                1150

CAT GAG ACT CCT CCA CAT CTC ACG TCC TAGGAATCTA CTTTCCTGTA            3503
His Glu Thr Pro Pro His Leu Thr Ser
        1155                1160

TATCTCCACA ATTACGAGAT TGGTTTTGCT TTTGCCTATG AATCTACTGG CATGGGAACA    3563

AGTTCTCTTC AGCTCTGGGC TAGCCTGGGA AACTTCCCAG AAATGATGCC CTACCTCCTG    3623

AGCTGGGAGA TTTTTATGGT TTGCCCATGT GTCAGATTTC AGTGCTGATC CACTTTTTTT    3683

GCAAGAGCAG GAATGGGGTC AGCATAAATT TACATATGGA TAAGAACTAA CACAAGACTG    3743

AGTAATATGC TCAATATTCA ATGTATTGCT TGTATAAATT TTTAAAAAAT AAAATGAAAN    3803
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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1161 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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Met Val Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser
 1               5                  10                  15

Cys His Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu
            20                  25                  30

Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg
        35                  40                  45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
    50                  55                  60

Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu
65                  70                  75                  80

Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
                85                  90                  95

Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala
            100                 105                 110

Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
        115                 120                 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro
    130                 135                 140

Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145                 150                 155                 160

Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys
                165                 170                 175

Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met
            180                 185                 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
        195                 200                 205

Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln
    210                 215                 220

Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu
225                 230                 235                 240

Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile
                245                 250                 255

Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His
            260                 265                 270

Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
        275                 280                 285
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Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp
385 390 395 400

Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly
465 470 475 480

Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys
485 490 495

Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
610 615 620

Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625 630 635 640

Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
725 730 735

Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
740 745 750

Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
755 760 765

Cys Lys Gln Glu Leu Leu Cys Glu Gly Asn Leu Gly Val Ser Phe Asn
770 775 780

Phe Ser Gly Leu Gln Val Leu Glu Val Gly Ser Ser Pro Glu Leu Thr
785 790 795 800

Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
805 810 815

Ile Lys Phe Tyr Tyr Pro Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg
820 825 830

Ala Gln Gln Pro His Pro Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
835 840 845

Pro Thr Gly Gln Glu Ser Leu Arg Ser Ser Ser Cys Ser Ile Asn His
850 855 860

Pro Ile Phe Arg Glu Gly Ala Lys Ala Thr Phe Met Ile Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Ser
885 890 895

Ala Ser Ser Glu Asn Asn Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln
900 905 910

Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln
915 920 925

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Glu Asp Ser Thr Lys His Phe Asn Phe Ser Ser Ser His Gly Glu Arg
    930                 935                 940

Gln Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945                 950                 955                 960

Thr Leu Ala Ile Ser Val Asn Phe Trp Val Pro Ile Leu Leu Asn Gly
                965                 970                 975

Val Ala Val Trp Asp Val Thr Leu Arg Ser Pro Ala Gln Gly Val Ser
            980                 985                 990

Cys Val Ser Gln Arg Glu Pro Pro Gln His Ser Asp Leu Leu Thr Gln
        995                 1000                1005

Ile Gln Gly Arg Ser Val Leu Asp Cys Ala Ile Ala Asp Cys Leu His
    1010                1015                1020

Leu Arg Cys Asp Ile Pro Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe
1025                1030                1035                1040

Ile Leu Lys Gly Asn Leu Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln
                1045                1050                1055

Lys Lys Val Leu Leu Leu Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser
            1060                1065                1070

Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
        1075                1080                1085

Ser Thr Met Leu Glu Glu Tyr Val Val Tyr Glu Pro Val Phe Leu Met
    1090                1095                1100

Val Phe Ser Ser Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Val
1105                1110                1115                1120

Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu
                1125                1130                1135

Asp Leu Pro Ser Ala Asp Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn
            1140                1145                1150

His Glu Thr Pro Pro His Leu Thr Ser
        1155                1160
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(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 40..3525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

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AGCTTTACAG CTCTCTACTT CTCAGTGCAC TGCTCAGTG ATG GCC GGT GGA GTT          54
                                            Met Ala Gly Gly Val
                                              1               5

GTG ATC CTC CTG TGT GGC TGG GTC CTG GCT TCC TGT CAT GGG TCT AAC         102
Val Ile Leu Leu Cys Gly Trp Val Leu Ala Ser Cys His Gly Ser Asn
                10                  15                  20

CTG GAT GTG GAG GAA CCC ATC GTG TTC AGA GAG GAT GCA GCC AGC TTT         150
Leu Asp Val Glu Glu Pro Ile Val Phe Arg Glu Asp Ala Ala Ser Phe
            25                  30                  35

GGA CAG ACT GTG GTG CAG TTT GGT GGA TCT CGA CTC GTG GTG GGA GCC         198
Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala
        40                  45                  50

CCT CTG GAG GCG GTG GCA GTC AAC CAA ACA GGA CGG TTG TAT GAC TGT         246
Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys
    55                  60                  65

GCA CCT GCC ACT GGC ATG TGC CAG CCC ATC GTA CTG CGC AGT CCC CTA         294
Ala Pro Ala Thr Gly Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu
70                  75                  80                  85

GAG GCA GTG AAC ATG TCC CTG GGC CTG TCT CTG GTG ACT GCC ACC AAT         342
Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn
                90                  95                  100

AAC GCC CAG TTG CTG GCT TGT GGT CCA ACT GCA CAG AGA GCT TGT GTG         390
Asn Ala Gln Leu Leu Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val
            105                 110                 115

AAG AAC ATG TAT GCG AAA GGT TCC TGC CTC CTT CTC GGC TCC AGC TTG         438
Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu
        120                 125                 130

CAG TTC ATC CAG GCA GTC CCT GCC TCC ATG CCA GAG TGT CCA AGA CAA         486
Gln Phe Ile Gln Ala Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln
    135                 140                 145

GAG ATG GAC ATT GCT TTC CTG ATT GAT GGT TCT GGC AGC ATT AAC CAA         534
Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln
150                 155                 160                 165

AGG GAC TTT GCC CAG ATG AAG GAC TTT GTC AAA GCT TTG ATG GGA GAG         582
Arg Asp Phe Ala Gln Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu
                170                 175                 180

TTT GCG AGC ACC AGC ACC TTG TTC TCC CTG ATG CAA TAC TCG AAC ATC         630
Phe Ala Ser Thr Ser Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile
            185                 190                 195

CTG AAG ACC CAT TTT ACC TTC ACT GAA TTC AAG AAC ATC CTG GAC CCT         678
Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro
        200                 205                 210

CAG AGC CTG GTG GAT CCC ATT GTC CAG CTG CAA GGC CTG ACC TAC ACA         726
Gln Ser Leu Val Asp Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr
    215                 220                 225
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GCC ACA GGC ATC CGG ACA GTG ATG GAA GAG CTA TTT CAT AGC AAG AAT          774
Ala Thr Gly Ile Arg Thr Val Met Glu Glu Leu Phe His Ser Lys Asn
230                 235                 240                 245

GGG TCC CGT AAA AGT GCC AAG AAG ATC CTC CTT GTC ATC ACA GAT GGG          822
Gly Ser Arg Lys Ser Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly
                250                 255                 260

CAG AAA TAC AGA GAC CCC CTG GAG TAT AGT GAT GTC ATT CCC GCC GCA          870
Gln Lys Tyr Arg Asp Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala
            265                 270                 275

GAC AAA GCT GGC ATC ATT CGT TAT GCT ATT GGG GTG GGA GAT GCC TTC          918
Asp Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe
        280                 285                 290

CAG GAG CCC ACT GCC CTG AAG GAG CTG AAC ACC ATT GGC TCA GCT CCC          966
Gln Glu Pro Thr Ala Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro
    295                 300                 305

CCA CAG GAC CAC GTG TTC AAG GTA GGC AAC TTT GCA GCA CTT CGC AGC         1014
Pro Gln Asp His Val Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser
310                 315                 320                 325

ATC CAG AGG CAA CTT CAG GAG AAA ATC TTC GCC ATT GAG GGA ACT CAA         1062
Ile Gln Arg Gln Leu Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln
                330                 335                 340

TCA AGG TCA AGT AGT TCC TTT CAG CAC GAG ATG TCA CAA GAA GGT TTC         1110
Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe
            345                 350                 355

AGT TCA GCT CTC ACA TCG GAT GGA CCC GTT CTG GGG GCC GTG GGA AGC         1158
Ser Ser Ala Leu Thr Ser Asp Gly Pro Val Leu Gly Ala Val Gly Ser
        360                 365                 370

TTC AGC TGG TCC GGA GGT GCC TTC TTA TAT CCC CCA AAT ACG AGA CCC         1206
Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro
    375                 380                 385

ACC TTT ATC AAC ATG TCT CAG GAG AAT GTG GAC ATG AGA GAC TCC TAC         1254
Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr
390                 395                 400                 405

CTG GGT TAC TCC ACC GCA GTG GCC TTT TGG AAG GGG GTT CAC AGC CTG         1302
Leu Gly Tyr Ser Thr Ala Val Ala Phe Trp Lys Gly Val His Ser Leu
                410                 415                 420

ATC CTG GGG GCC CCG CGT CAC CAG CAC ACG GGG AAG GTT GTC ATC TTT         1350
Ile Leu Gly Ala Pro Arg His Gln His Thr Gly Lys Val Val Ile Phe
            425                 430                 435

ACC CAG GAA GCC AGG CAT TGG AGG CCC AAG TCT GAA GTC AGA GGG ACA         1398
Thr Gln Glu Ala Arg His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr
        440                 445                 450

CAG ATC GGC TCC TAC TTC GGG GCC TCT CTC TGT TCT GTG GAC GTG GAT         1446
Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp
    455                 460                 465
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AGA GAT GGC AGC ACY GAC CTG GTC CTG ATC GGA GCC CCC CAT TAC TAT      1494
Arg Asp Gly Ser Xaa Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr
470                 475                 480                 485

GAG CAG ACC CGA GGG GGG CAG GTC TCA GTG TTC CCC GTG CCC GGT GTG      1542
Glu Gln Thr Arg Gly Gly Gln Val Ser Val Phe Pro Val Pro Gly Val
                490                 495                 500

AGG GGC AGG TGG CAG TGT GAG GCC ACC CTC CAC GGG GAG CAG GGC CAT      1590
Arg Gly Arg Trp Gln Cys Glu Ala Thr Leu His Gly Glu Gln Gly His
            505                 510                 515

CCT TGG GGC CGC TTT GGG GTG GCT CTG ACA GTG CTG GGG GAC GTA AAC      1638
Pro Trp Gly Arg Phe Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn
        520                 525                 530

GGG GAC AAT CTG GCA GAC GTG GCT ATT GGT GCC CCT GGA GAG GAG GAG      1686
Gly Asp Asn Leu Ala Asp Val Ala Ile Gly Ala Pro Gly Glu Glu Glu
    535                 540                 545

AGC AGA GGT GCT GTC TAC ATA TTT CAT GGA GCC TCG AGA CTG GAG ATC      1734
Ser Arg Gly Ala Val Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile
550                 555                 560                 565

ATG CCC TCA CCC AGC CAG CGG GTC ACT GGC TCC CAG CTC TCC CTG AGA      1782
Met Pro Ser Pro Ser Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg
                570                 575                 580

CTG CAG TAT TTT GGG CAG TCA TTG AGT GGG GGT CAG GAC CTT ACA CAG      1830
Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln
            585                 590                 595

GAT GGC CTG GTG GAC CTG GCC GTG GGA GCC CAG GGG CAC GTA CTG CTG      1878
Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln Gly His Val Leu Leu
        600                 605                 610

CTC AGG AGT CTG CCT CTG CTG AAA GTG GAG CTC TCC ATA AGA TTC GCC      1926
Leu Arg Ser Leu Pro Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala
    615                 620                 625

CCC ATG GAG GTG GCA AAG GCT GTG TAC CAG TGC TGG GAA AGG ACT CCC      1974
Pro Met Glu Val Ala Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro
630                 635                 640                 645

ACT GTC CTC GAA GCT GGA GAG GCC ACT GTC TGT CTC ACT GTC CAC AAA      2022
Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys Leu Thr Val His Lys
                650                 655                 660

GGC TCA CCT GAC CTG TTA GGT AAT GTC CAA GGC TCT GTC AGG TAT GAT      2070
Gly Ser Pro Asp Leu Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp
            665                 670                 675

CTG GCG TTA GAT CCG GGC CGC CTG ATT TCT CGT GCC ATT TTT GAT GAG      2118
Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu
        680                 685                 690

ACT AAG AAC TGC ACT TTG ACG GGA AGG AAG ACT CTG GGG CTT GGT GAT      2166
Thr Lys Asn Cys Thr Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp
    695                 700                 705
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CAC TGC GAA ACA GTG AAG CTG CTT TTG CCG GAC TGT GTG GAA GAT GCA      2214
His Cys Glu Thr Val Lys Leu Leu Leu Pro Asp Cys Val Glu Asp Ala
710                 715                 720                 725

GTG AGC CCT ATC ATC CTG CGC CTC AAC TTT TCC CTG GTG AGA GAC TCT      2262
Val Ser Pro Ile Ile Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser
                730                 735                 740

GCT TCA CCC AGG AAC CTG CAT CCT GTG CTG GCT GTG GGC TCA CAA GAC      2310
Ala Ser Pro Arg Asn Leu His Pro Val Leu Ala Val Gly Ser Gln Asp
            745                 750                 755

CAC ATA ACT GCT TCT CTG CCG TTT GAG AAG AAC TGT AAG CAA GAA CTC      2358
His Ile Thr Ala Ser Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu
        760                 765                 770

CTG TGT GAG GGG GAC CTG GGC ATC AGC TTT AAC TTC TCA GGC CTG CAG      2406
Leu Cys Glu Gly Asp Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln
    775                 780                 785

GTC TTG GTG GTG GGA GGC TCC CCA GAG CTC ACT GTG ACA GTC ACT GTG      2454
Val Leu Val Val Gly Gly Ser Pro Glu Leu Thr Val Thr Val Thr Val
790                 795                 800                 805

TGG AAT GAG GGT GAG GAC AGC TAT GGA ACT TTA GTC AAG TTC TAC TAC      2502
Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr
                810                 815                 820

CCA GCA GGG CTA TCT TAC CGA CGG GTA ACA GGG ACT CAG CAA CCT CAT      2550
Pro Ala Gly Leu Ser Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His
            825                 830                 835

CAG TAC CCA CTA CGC TTG GCC TGT GAG GCT GAG CCC GCT GCC CAG GAG      2598
Gln Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu Pro Ala Ala Gln Glu
        840                 845                 850

GAC CTG AGG AGC AGC AGC TGT AGC ATT AAT CAC CCC ATC TTC CGA GAA      2646
Asp Leu Arg Ser Ser Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu
    855                 860                 865

GGT GCA AAG ACC ACC TTC ATG ATC ACA TTC GAT GTC TCC TAC AAG GCC      2694
Gly Ala Lys Thr Thr Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala
870                 875                 880                 885

TTC CTA GGA GAC AGG TTG CTT CTG AGG GCC AAA GCC AGC AGT GAG AAT      2742
Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Lys Ala Ser Ser Glu Asn
                890                 895                 900

AAT AAG CCT GAT ACC AAC AAG ACT GCC TTC CAG CTG GAG CTC CCA GTG      2790
Asn Lys Pro Asp Thr Asn Lys Thr Ala Phe Gln Leu Glu Leu Pro Val
            905                 910                 915

AAG TAC ACC GTC TAT ACC CTG ATC AGT AGG CAA GAA GAT TCC ACC AAC      2838
Lys Tyr Thr Val Tyr Thr Leu Ile Ser Arg Gln Glu Asp Ser Thr Asn
        920                 925                 930

CAT GTC AAC TTT TCA TCT TCC CAC GGG GGG AGA AGG CAA GAA GCC GCA      2886
His Val Asn Phe Ser Ser Ser His Gly Gly Arg Arg Gln Glu Ala Ala
    935                 940                 945
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CAT CGC TAT CGT GTG AAT AAC CTG AGT CCA CTG AAG CTG GCC GTC AGA          2934
His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu Lys Leu Ala Val Arg
950                 955                 960                 965

GTT AAC TTC TGG GTC CCT GTC CTT CTG AAC GGT GTG GCT GTG TGG GAC          2982
Val Asn Phe Trp Val Pro Val Leu Leu Asn Gly Val Ala Val Trp Asp
                970                 975                 980

GTG ACT CTG AGC AGC CCA GCA CAG GGT GTC TCC TGC GTG TCC CAG ATG          3030
Val Thr Leu Ser Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met
            985                 990                 995

AAA CCT CCT CAG AAT CCC GAC TTT CTG ACC CAG ATT CAG AGA CGT TCT          3078
Lys Pro Pro Gln Asn Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser
        1000                1005                1010

GTG CTG GAC TGC TCC ATT GCT GAC TGC CTG CAC TTC CGC TGT GAC ATC          3126
Val Leu Asp Cys Ser Ile Ala Asp Cys Leu His Phe Arg Cys Asp Ile
    1015                1020                1025

CCC TCC TTG GAC ATC CAG GAT GAA CTT GAC TTC ATT CTG AGG GGC AAC          3174
Pro Ser Leu Asp Ile Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn
1030                1035                1040                1045

CTC AGC TTC GGC TGG GTC AGT CAG ACA TTG CAG GAA AAG GTG TTG CTT          3222
Leu Ser Phe Gly Trp Val Ser Gln Thr Leu Gln Glu Lys Val Leu Leu
                1050                1055                1060

GTG AGT GAG GCT GAA ATC ACT TTC GAC ACA TCT GTG TAC TCC CAG CTG          3270
Val Ser Glu Ala Glu Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu
            1065                1070                1075

CCA GGA CAG GAG GCA TTT CTG AGA GCC CAG GTG GAG ACA ACG TTA GAA          3318
Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu
        1080                1085                1090

GAA TAC GTG GTC TAT GAG CCC ATC TTC CTC GTG GCG GGC AGC TCG GTG          3366
Glu Tyr Val Val Tyr Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val
    1095                1100                1105

GGA GGT CTG CTG TTA CTG GCT CTC ATC ACA GTG GTA CTG TAC AAG CTT          3414
Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu
1110                1115                1120                1125

GGC TTC TYC AAA CGT CAG TAC AAA GAA ATG CTG GAC GGC AAG GCT GCA          3462
Gly Phe Xaa Lys Arg Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala
                1130                1135                1140

GAT CCT GTC ACA GCC GGC CAG GCA GAT TTC GGC TGT GAG ACT CCT CCA          3510
Asp Pro Val Thr Ala Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro
            1145                1150                1155

TAT CTC GTG AGC TAGGAATCCA CTCTCCTGCC TATCTCTGCA ATGAAGATTG              3562
Tyr Leu Val Ser
        1160

GTCCTGCCTA TGAGTCTACT GGCATGGGAA CGAGT                                   3597
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Met Ala Gly Gly Val Val Ile Leu Leu Cys Gly Trp Val Leu Ala Ser
 1               5                  10                  15

Cys His Gly Ser Asn Leu Asp Val Glu Glu Pro Ile Val Phe Arg Glu
            20                  25                  30

Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg
        35                  40                  45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
    50                  55                  60

Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly Met Cys Gln Pro Ile Val
65                  70                  75                  80

Leu Arg Ser Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
                85                  90                  95

Val Thr Ala Thr Asn Asn Ala Gln Leu Leu Ala Cys Gly Pro Thr Ala
            100                 105                 110

Gln Arg Ala Cys Val Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
        115                 120                 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Val Pro Ala Ser Met Pro
    130                 135                 140

Glu Cys Pro Arg Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145                 150                 155                 160

Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln Met Lys Asp Phe Val Lys
                165                 170                 175

Ala Leu Met Gly Glu Phe Ala Ser Thr Ser Thr Leu Phe Ser Leu Met
            180                 185                 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
        195                 200                 205

Asn Ile Leu Asp Pro Gln Ser Leu Val Asp Pro Ile Val Gln Leu Gln
    210                 215                 220

Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg Thr Val Met Glu Glu Leu
225                 230                 235                 240

Phe His Ser Lys Asn Gly Ser Arg Lys Ser Ala Lys Lys Ile Leu Leu
                245                 250                 255

Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp Pro Leu Glu Tyr Ser Asp
            260                 265                 270
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Val Ile Pro Ala Ala Asp Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
275 280 285

Val Gly Asp Ala Phe Gln Glu Pro Thr Ala Leu Lys Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Pro Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr Ser Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Pro Asn Thr Arg Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp
385 390 395 400

Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr Ala Val Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ala Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Val Asp Arg Asp Gly Ser Xaa Asp Leu Val Leu Ile Gly
465 470 475 480

Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Phe
485 490 495

Pro Val Pro Gly Val Arg Gly Arg Trp Gln Cys Glu Ala Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Val Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Asn Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Ser Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

Ser Arg Leu Glu Ile Met Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Glu Leu
610 615 620

Ser Ile Arg Phe Ala Pro Met Glu Val Ala Lys Ala Val Tyr Gln Cys
625 630 635 640

Trp Glu Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val His Lys Gly Ser Pro Asp Leu Leu Gly Asn Val Gln Gly
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Gly Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Val Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Ser Pro Ile Ile Leu Arg Leu Asn Phe Ser
725 730 735

Leu Val Arg Asp Ser Ala Ser Pro Arg Asn Leu His Pro Val Leu Ala
740 745 750

Val Gly Ser Gln Asp His Ile Thr Ala Ser Leu Pro Phe Glu Lys Asn
755 760 765

Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp Leu Gly Ile Ser Phe Asn
770 775 780

Phe Ser Gly Leu Gln Val Leu Val Val Gly Gly Ser Pro Glu Leu Thr
785 790 795 800

Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
805 810 815

Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser Tyr Arg Arg Val Thr Gly
820 825 830

Thr Gln Gln Pro His Gln Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
835 840 845

Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser Ser Cys Ser Ile Asn His
850 855 860

Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr Phe Met Ile Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Lys
885 890 895

Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr Asn Lys Thr Ala Phe Gln
900 905 910

Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Leu Ile Ser Arg Gln
915 920 925

Glu Asp Ser Thr Asn His Val Asn Phe Ser Ser Ser His Gly Gly Arg
930 935 940

Arg Gln Glu Ala Ala His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945 950 955 960

Lys Leu Ala Val Arg Val Asn Phe Trp Val Pro Val Leu Leu Asn Gly
965 970 975

Val Ala Val Trp Asp Val Thr Leu Ser Ser Pro Ala Gln Gly Val Ser
980 985 990

Cys Val Ser Gln Met Lys Pro Pro Gln Asn Pro Asp Phe Leu Thr Gln
995 1000 1005

Ile Gln Arg Arg Ser Val Leu Asp Cys Ser Ile Ala Asp Cys Leu His
1010 1015 1020

Phe Arg Cys Asp Ile Pro Ser Leu Asp Ile Gln Asp Glu Leu Asp Phe
1025 1030 1035 1040

Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp Val Ser Gln Thr Leu Gln
1045 1050 1055

Glu Lys Val Leu Leu Val Ser Glu Ala Glu Ile Thr Phe Asp Thr Ser
1060 1065 1070

Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
1075 1080 1085

Glu Thr Thr Leu Glu Glu Tyr Val Val Tyr Glu Pro Ile Phe Leu Val
1090 1095 1100

Ala Gly Ser Ser Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Val
1105 1110 1115 1120

Val Leu Tyr Lys Leu Gly Xaa Xaa Lys Arg Gln Tyr Lys Glu Met Leu
1125 1130 1135

Asp Gly Lys Ala Ala Asp Pro Val Thr Xaa Gly Gln Ala Asp Phe Gly
1140 1145 1150

Cys Glu Thr Pro Pro Tyr Leu Val Ser
1155 1160

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CCTGTCATGG GTCTAACCTG 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGGTTAGACC CATGACAGG 19

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCCTTGCAG CTGGACAATG 20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCAAAGCTGG CTGCATCCTC TC 22

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGCCTGCCA CTGGCGTGTG C 21

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCAGATGAA GGACTTCGTC AA 22

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCTGGGATCA TTCGCTATGC 20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CAATGGATGG ACCAGTTCTG G 21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGATCGGCT CCTACTTTGG 20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CATGGAGCCT CGAGACAGG 19

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CCACTGTCCT CGAAGCTGGA G 21

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTCGTCCTG TGCTGGCTGT GGGCTC 26

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CGCCTGGCAT GTGAGGCTGA G 21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCGTGATCAG TAGGCAGGAA G 21

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCACAGAGG GAACCTCC 18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCTCCTGAGT GAGGCTGAAA TCA 23

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAGATGCTGG ATCTACCATC TGC 23

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CTGAGCTGGG AGATTTTTAT GG 22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGGATCAGC ACTGAAATCT G 21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGTTTGAAGA AGCCAAGCTT G 21

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CACAGCGGAG GTGCAGGCAG 20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCACTGCTT GCGCTGGC 18

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CGGTAAGATA GCTCTGCTGG 20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAGCCCACAG CCAGCACAGG 20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATCCAACGC CAGATCATAC C 21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
CACGGCCAGG TCCACCAGGC 20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CACGTCCCCT AGCACTGTCA G 21

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTGACGAAGT CCTTCATCTG GG 22

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAACTGCAAG CTGGAGCCCA G 21

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGGATGCTG CGAAGTGCTA C 21

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCCTTGGAGC TGGACGATGG C 21

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTAAGATCTC CAGAGTGTCC AAGACAAGAG ATG 33

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTTCTCGAGT GTGAGAGCTG AACTGAAACC TTC 33

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CGCTGTGACG TCAGAGTTGA GTCCAAATAT GG 32

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GGTGACACTA TAGAATAGGG C 21

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AAGCAGGAGCTCCTGTGT 18

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 61..852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
TGATCTCCCT CCAGGCCACT GTTCCCTCTC CACTTCCCCT CACCGCTGCA CTGCTCAGAG       60

ATG GCC CTT GGG GCT GTG GTC CTC CTT GGG GTC CTG GCT TCT TAC CAC       108
Met Ala Leu Gly Ala Val Val Leu Leu Gly Val Leu Ala Ser Tyr His
  1               5                  10                  15

GGA TTC AAC TTG GAC GTG ATG AGC GGT GAT CTT CCA GGA AGA CGC AGC       156
Gly Phe Asn Leu Asp Val Met Ser Gly Asp Leu Pro Gly Arg Arg Ser
             20                  25                  30

GGG CTT CGG GCA GAG CGT GAT GCA GTT TGG GGA TCT CGA CTC GTG GTG       204
Gly Leu Arg Ala Glu Arg Asp Ala Val Trp Gly Ser Arg Leu Val Val
         35                  40                  45

GGA GCC CCC CTG GCG GTG GTG TCG GCC AAC CAC ACA GGA CGG CTG TAC       252
Gly Ala Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg Leu Tyr
     50                  55                  60

GAG TGT GCG CCT GCC TCC GGC ACC TGC ACG CCC ATT TTC CCA TTC ATG       300
Glu Cys Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro Phe Met
 65                  70                  75                  80

CCC CCC GAA GCC GTG AAC ATG TCC CTG GGC CTG TCC CTG GCA GCC TCC       348
Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Ser
                 85                  90                  95

CCC AAC CAT TCC CAG CTG CTG GCT TGT GGC CCG ACC GTG CAT AGA GCC       396
Pro Asn His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His Arg Ala
            100                 105                 110
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TGC GGG GAG GAC GTG TAC GCC CAG GGT TTC TGT GTG CTG CTG GAT GCC        444
Cys Gly Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu Asp Ala
        115                 120                 125

CAC GCA CAG CCC ATC GGG ACT GTG CCA GCT GCC CTG CCC GAG TGC CCA        492
His Ala Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu Cys Pro
    130                 135                 140

GAT CAA GAG ATG GAC ATT GTC TTC CTG ATT GAC GGC TCT GGC AGC ATT        540
Asp Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile
145                 150                 155                 160

AGC TCA AAT GAC TTC CGC AAG ATG AAG GAC TTT GTC AGA GCT GTG ATG        588
Ser Ser Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala Val Met
                165                 170                 175

GAC CAG TTC AAG GAC ACC AAC ACC CAG TTC TCG CTG ATG CAG TAC TCC        636
Asp Gln Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln Tyr Ser
            180                 185                 190

AAT GTG CTG GTG ACA CAT TTC ACC TTC AGC AGC TTC CGG AAC AGC TCC        684
Asn Val Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn Ser Ser
        195                 200                 205

AAT CCT CAG GGC CTA GTG GAG CCC ATT GTG CAG CTG ACA GGC CTC ACG        732
Asn Pro Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly Leu Thr
    210                 215                 220

TTC ACG GCC ACA GGG ATC CTG AAA GTG GTG ACA GAG CTG TTT CAA ACC        780
Phe Thr Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe Gln Thr
225                 230                 235                 240

AAG AAC GGG GCC CGC GAA AGT GCC AAG AAG ATC CTC ATC GTC ATC ACA        828
Lys Asn Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val Ile Thr
                245                 250                 255

GAT GGG CAG AAG TAC AAA GCG GCA                                       852
Asp Gly Gln Lys Tyr Lys Ala Ala
            260
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Met Ala Leu Gly Ala Val Val Leu Leu Gly Val Leu Ala Ser Tyr His
  1               5                  10                  15

Gly Phe Asn Leu Asp Val Met Ser Gly Asp Leu Pro Gly Arg Arg Ser
            20                  25                  30

Gly Leu Arg Ala Glu Arg Asp Ala Val Trp Gly Ser Arg Leu Val Val
        35                  40                  45
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Gly Ala Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg Leu Tyr
     50                  55                  60

Glu Cys Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro Phe Met
 65                  70                  75                  80

Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Ser
                 85                  90                  95

Pro Asn His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His Arg Ala
            100                 105                 110

Cys Gly Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu Asp Ala
        115                 120                 125

His Ala Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu Cys Pro
    130                 135                 140

Asp Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile
145                 150                 155                 160

Ser Ser Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala Val Met
                165                 170                 175

Asp Gln Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln Tyr Ser
            180                 185                 190

Asn Val Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn Ser Ser
        195                 200                 205

Asn Pro Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly Leu Thr
    210                 215                 220

Phe Thr Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe Gln Thr
225                 230                 235                 240

Lys Asn Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val Ile Thr
                245                 250                 255

Asp Gly Gln Lys Tyr Lys Ala Ala
            260
```

WHAT IS CLAIMED IS:

1. A purified and isolated α_d polynucleotide consisting essentially of human α_d protein coding sequence set out in SEQ ID NO: 1.

2. The polynucleotide of claim 1 which is a DNA molecule.

3. The DNA molecule of claim 2 which is a cDNA molecule.

4. The DNA molecule of claim 2 which is a genomic DNA molecule.

5. The DNA molecule of claim 2 which is a wholly or partially chemically synthesized DNA molecule.

6. A full length purified and isolated α_d-encoding polynucleotide selected from the group consisting of:

a) the human DNA sequence set out in SEQ ID NO: 1, and

b) a DNA molecule which hybridizes under stringent conditions to the noncoding strand of the protein coding portion of the DNA of a).

7. A DNA molecule encoding the human α_d amino acid sequence set out in SEQ ID NO: 2.

8. A DNA expression construct comprising a DNA molecule according to claim 2.

9. A host cell transformed with a DNA molecule according to claim 2.

10. A method for producing an α_d polypeptide comprising growing a host cell according to claim 9 in a suitable medium and isolating α_d polypeptide from said host cell or the medium of its growth.

11. Purified and isolated α_d polypeptide consisting essentially of the human α_d amino acid sequence set out in SEQ ID NO: 2.

12. A polypeptide capable of specifically binding to α_d.

13. A polypeptide according to claim 12 which is an antibody.

14. An antibody according to claim 13 which is a monoclonal antibody.

15. An anti-idiotype antibody specific for the monoclonal antibody of claim 14.

16. A hybridoma cell line producing the monoclonal antibody according to claim 14.

17. A purified and isolated α_d extracellular domain polypeptide fragment comprising amino acids 17 to 1108 of the human α_d amino acid sequence set out in SEQ ID NO: 2.

18. A purified and isolated α_d I domain polypeptide fragment comprising amino acids 145 to 355 of the human α_d amino acid sequence set out in SEQ ID NO: 2.

19. A fusion protein comprising α_d extracellular domain polypeptide amino acids 17 to 1108 of SEQ ID NO: 2 and human immunoglobulin constant domain sequences.

20. A purified and isolated murine polynucleotide consisting essentially of the α subunit protein coding sequence set out in SEQ ID NO: 45.

21. A method for isolating a polynucleotide encoding a protein that binds to α_d comprising the steps of:

a) transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and an activating domain;

b) expressing in said host cells a first hybrid DNA sequence encoding a first fusion of part or all of α_d and either the DNA binding domain or the activating domain of said transcription factor;

c) expressing in said host cells a library of second hybrid DNA sequences encoding second fusions of part or all of putative α_d binding proteins and the DNA binding domain or activating domain of said transcription factor which is not incorporated in said first fusion;

d) detecting binding of an α_d binding protein to α_d in a particular host cell by detecting the production of reporter gene product in said host cell; and

e) isolating second hybrid DNA sequences encoding α_d binding protein from said particular host cell.

22. A method for identifying a compound capable of reacting specifically with α_d and of modulating the interaction of binding partners α_d and ICAM-R comprising the steps of:

a) immobilizing α_d or a fragment thereof, or ICAM-R or a fragment thereof, on a solid support coated or impregnated with a fluorescent agent;

b) labelling the non-immobilized binding partner with a compound capable of exciting said fluorescent agent;

c) contacting said immobilized binding partner with said labelled binding partner in the presence and absence of a putative modulator compound capable of specifically reacting with α_d;

d) detecting light emission by said fluorescent agent; and

e) identifying modulating compounds as those compounds that affect the emission of light by said fluorescent agent in comparison to the emission of light by said fluorescent agent in the absence of said modulating compound.

23. A purified and isolated α_d extracellular domain polypeptide fragment comprising about amino acid 127 to about amino acid 353 of the human α_d amino acid sequence set out in SEQ ID NO: 2.

24. A fusion protein comprising the polypeptide fragment of claim 23 and human immunoglobulin constant region sequences.

25. A purified and isolated α_d extracellular domain polypeptide fragment comprising about amino acid 17 to about amino acid 603 of the human α_d amino acid sequence set out in SEQ ID NO: 2.

26. A fusion protein comprising the polypeptide fragment of claim 25 and human immunoglobulin constant region sequences.

```
αD      TF-GT--VLL LSVLASYHGF NLDVEEPTIF QEDAGGFGQS VVQFGGSRLV   47
CD11B   MA-LR--VLL LTALTLCHGF NLDTENAMTF QENARGFGQS VVQLQGSRVV   47
CD11c   MTRTRAALLL FTALATSLGF NLDTEELTAF RVDSAGFGDS VVQYANSWVV   50

αD      VGAPLEVVAA NQTGRLYDCA AATGMCQPIP LHIRPEAVNM SLGLTLAAST   97
CD11B   VGAPQEIVAA NQRGSLYQCD YSTGSCEPIR LQVPVEAVNM SLGLSLAATT   97
CD11c   VGAPQKIIAA NQIGGLYQCG YSTGACEPIG LQVPPEAVNM SLGLSLASTT  100

αD      NGSRLLACGP TLHRVCGENS YSKGSCLLLG SR-WEIIQTV PDATPECPHQ  146
CD11B   SPPQLLACGP TVHQTCSENT YVKGLCFLFG SNLRQQPQKF PEALRGCPQE  147
CD11c   SPSQLLACGP TVHHECGRNM YLTGLCFLLG PT--QLTQRL PVSRQECPRQ  148

αD      EMDIVFLIDG SGSIDQNDFN QMKGFVQAVM GQFEGTDTLF ALMQYSNLLK  196
CD11B   DSDIAFLIDG SGSIIPHDFR RMKEFVSTVM EQLKKSKTLF SLMQYSEEFR  197
CD11c   EQDIVFLIDG SGSISSRNFA TMMNFVRAVI SQFQRPSTQF SLMQFSNKFQ  198

αD      IHFTFTQFRT SPSQQSLVDP IVQLKGLTFT ATGILTVVTQ LFHHKNGARK  246
CD11B   IHFTFKEFQN NPNPRSLVKP ITQLLGRTHT ATGIRKVVRE LFNITNGARK  247
CD11c   THFTFEEFRR TSNPLSLLAS VHQLQGFTYT ATAIQNVVHR LFHASYGARR  248

αD      SAKKILIVIT DGQKYKDPLE YSDVIPQAEK AGIIRYAIGV GHAFQGPTAR  296
CD11B   NAFKILVVIT DGEKFGDPLG YEDVIPEADR EGVIRYVIGV GDAFRSEKSR  297
CD11c   DAIKILIVIT DGKKEGDSLD YKDVIPMADA AGIIRYAIGV GLAFQNRNSW  298
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FIGURE 1A

αD	QELNTISSAP PQDHVFKVDN FAALGSIQKQ LQEKIYAVEG TQSRASSSFQ	346
CD11B	QELNTIASKP PRDHVFQVNN FEALKTIQNQ LREKIFAIEG TQTGSSSSFE	347
CD11c	KELNDIASKP SQEHIFKVED FDALKDIQNQ LKEKIFAIEG TETISSSSFE	348
αD	HEMSQEGFST ALTMDGLFLG AVGSFSWSGG AFLYPPNMSP TFINMSQENV	396
CD11B	HEMSQEGFSA AITSNGPLLS TVGSYDWAGG VFLYTSKEKS TFINMTRVDS	397
CD11c	LEMAQEGFSA VFTPDGPVLG AVGSFTWSGG AFLYPPNMSP TFINMSQENV	398
αD	DMRDSYLGYS TELALWKGVQ NLVLGAPRYQ HTGKAVIFTQ VSRQWRKKAE	446
CD11B	DMNDAYLGYA AAIILRNRVQ SLVLGAPRYQ HIGLVAMFRQ NTGMWESNAN	447
CD11c	DMRDSYLGYS TELALWKGVQ SLVLGAPRYQ HIGKAVIFIQ VSRQWRMKAE	448
αD	VTGTQIGSYF GASLCSVDVD SDGSTDLILI GAPHYYEQTR GGQVSVCPLP	496
CD11B	VKGTQIGAYF GASLCSVDVD SNGSTDLVLI GAPHYYEQTR GGQVSVCPLP	497
CD11c	VIGTQIGSYF GASLCSVDVD TDGSTDLVLI GAPHYYEQTR GGQVSVCPLP	498
αD	RGQRVQWQCD AVLRGEQGHP WGRFGAALTV LGDVNEDKLI DVAIGAPGEQ	546
CD11B	RGQRARWQCD AVLYGEQGQP WGRFGAALTV LGDVNGDKLT DVAIGAPGEE	547
CD11c	RGWRRWW-CD AVLYGEQGHP WGRFGAALTV LGDVNGDKLT DVVIGAPGEE	547
αD	ENRGAVYLFH GASESGISPS HSQRIASSQL SPRLQYFGQA LSGGQDLTQD	596
CD11B	DNRGAVYLFH GTSGSGISPS HSQRIAGSKL SPRLQYFGQS LSGGQDLTMD	597
CD11c	ENRGAVYLFH GVLGPSISPS HSQRIAGSQL SSRLQYFGQA LSGGQDLTQD	597

FIGURE 1B

27. A purified and isolated α_d extracellular domain polypeptide fragment comprising about amino acid 17 to about about amino acid 1029 of the human α_d amino acid sequence set out in SEQ ID NO: 2.

28. A fusion protein comprising the polypeptide fragment of claim 27 and immunoglobulin constant region sequences.

29. A purified and isolated murine polynucleotide comprising the α subunit protein coding sequence as set out in SEQ ID NO: 52.

30. A purified and isolated α_d polypeptide consisting essentially of the murine α_d amino acid sequence set out in SEQ ID NO: 53.

31. A purified and isolated rat polynucleotide comprising the α subunit protein coding sequence as set out in SEQ ID NO: 54.

32. A purified and isolated α_d polypeptide consisting essentially of the rat α_d amino acid sequence set out in SEQ ID NO: 55.

33. A purified and isolated polypeptide fragment comprising extracellular domain sequences of the polypeptide of claim 32.

34. A polypeptide capable of specifically binding to the polypeptide of claim 32.

35. A polypeptide according to claim 34 which is an antibody.

36. An antibody according to claim 35 which is a monoclonal antibody.

37. A rodent that does not express a functional α_d protein.

38. A rodent that expresses a variant α_d protein.

αD	GLMDLAVGAR GQVLLLRSLP VLKVGVAMRF SPVEVAKAVY RCWEEKPSAL	646
CD11B	GLVDLTVGAQ GHVLLLRSQP VLRVKAIMEF NPREVARNVF ECNDQVVKGK	647
CD11c	GLVDLAVGAR GQVLLLRTRP VLWVGVSMQF IPAEIPRSAF ECREQVVSEQ	647
αD	EAGDATVCLT IQKSSLDQL- -GDIQSSVRF DLALDPGRLT SRAIFNETKN	694
CD11B	EAGEVRVCLH VQKSTRDRLR EGQIQSVVTY DLALDSGRPH SRAVFNETKN	697
CD11c	TLVQSNICLY IDKRSKNLLG SRDLQSSVTL DLALAPGRLS PRAIFQETKN	697
αD	PTLTTRKTLG LGIHCETLKL LLPDCVEDVV SPIILHLNFS LVREPIPSPQ	744
CD11B	STRRQTQVLG LTQTCETLKL QLPNCIEDPV SPIVLRLNFS LVGTPLSAFG	747
CD11c	RSLSRVRVLG LKAHCENFNL LLPSCVEDSV IPIILRLNFT LVGKPLLAFR	747
αD	NLRPVLAVGS QDLFTASLPF EKNCGQDGLC EGDLGVTLSF SGLQTLTVGS	794
CD11B	NLRPVLAEDA QRLFTALFPF EKNCGNDNIC QDDLSITFSF MSLDCLVVGG	797
CD11c	NLRPMLAALA QRYFTASLPF EKNCGADHIC QDNLGISFSF PGLKSLLVGS	797
αD	SLELNVIVTV WNAGEDSYGT VVSLYYPAGL SHRRVSGAQK QPHQSALRLA	844
CD11B	PREFNVTVTV RNDGEDSYRT QVTFFFPLDL SYRKVSTLQN QRSQRSWRLA	847
CD11c	NLELNAEVMV WNDGEDSYGT TITFSHPAGL SYRYVAEGQK QGQLRSLHLT	847
αD	CETVPTED-- EGLRSSRCSV NHPIFHEGSN GTFIVTFDVS Y----KATLG	888
CD11B	CESASSTEVS GALKSTSCSI NHPIFPENSE ----VTFNIT FDVDSKASLG	893
CD11c	CCSA-PVGSQ GTW-STSCRI NHLIFRGGAQ ----ITFLAT FDVSPKAVGL	891

FIGURE 1C

```
αD      DRMLMRASAS SENNKASSSK ATFQLELPVK YAVYTMISRQ EESTKYFNFA   938
CD11B   NKLLLKANVT SENNMPRTNK TEFQLELPVK YAVYMVVTSH GVSTKYLNFT   943
CD11c   DRLLLIANVS SENNIPRTSK TIFQLELPVK YAVYIVVSSH EQFTKYLNFS   941

αD      TS-DEKKMKE AEHRYRVNNL SQRDLAISIN FWVPVLLNGV AVWDVVMEAP   987
CD11B   AS-ENTS-RV MQHQYQVSNL GQRSLPISLV FLVPVRLNQT VIWDRPQVTF   991
CD11c   ESEEKES-HV AMHRYQVNNL GQRDLPVSIN FWVPVELNQE AVWMDVEVSH   990

αD      SQSLP--CVS ERKPPQHSDF LTQISRSPML DCSIADCLQF RCDVPSFSVQ  1035
CD11B   SENLSSTCHT KERLPSHSDF LAELRKAPVV NCSIAVCQRI QCDIPFFGIQ  1041
CD11c   PQNPSLRCSS EKIAPPASDF LAHIQKNPVL DCSIAGCLRF RCDVPSFSVQ  1040

αD      EELDFTLKGN LSFGWVRETL QKKVLVVSVA EITFDTSVYS QLPGQEAFMR  1085
CD11B   EEFNATLKGN LSFDWYIKTS HNHLLIVSTA EILFNDSVFT LLPGQGAFVR  1091
CD11c   EELDFTLKGN LSFGWVRQIL QKKVSVVSVA EIIFDTSVYS QLPGQEAFMR  1090

αD      AQMEMVLEED EVYNAIPIIM GSSVGALLLL ALITATLYKL GFFKRHYKEM  1135
CD11B   SQTETKVEPF EVPNPLPLIV GSSVGGLLLL ALITAALYKL GFFKRQYKDM  1141
CD11c   AQTITVLEKY KVHNPIPLIV GSSIGGLLLL ALITAVLYKV GFFKRQYKEM  1140

αD      LEDKPED--- -----TATFS GDDFSCVAPN VPLS                   1161
CD11B   M---SEG--- -----GP--P GAE-----PQ ----                   1153
CD11c   M---EEANGQ IAPENGT--Q TPS-----PP SEK                    1163
```

FIGURE 1D

INTERNATIONAL SEARCH REPORT

In. .ational application No.
PCT/US94/14832

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 7.1, 69.1, 240.2, 252.3, 320.1; 530/350, 387.1, 387.2, 388.1, 388.22; 536/22.1, 23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

None

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, BIOSIS, CAS ONLINE, STN
search terms: human beta2 integrin, leukointegrin, leu cam, leukocyte integrin#, alphad, integrin, alphas

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CELL, Volume 72, issued 26 March 1993, Michishita et al., "A Novel Divalent Cation-Binding Site in the A Domain of the β2 Integrin CR3 (CD11b/CD18) Is Essential for Ligand Binding", pages 857-867, see entire document.	1-38
A	CELL, Volume 69, issued 03 April 1992, Hynes, "Integrins: Versatility, Modulation, and Signaling in Cell Adhesion", pages 11-25, see entire document.	1-38

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 11 APRIL 1995	Date of mailing of the international search report 17APR1995
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer Hyosuk Kim Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US94/14832

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	THE JOURNAL OF IMMUNOLOGY, Volume 150, Number 2, issued 13 January 1993, Fleming et al., "Structural Analysis of the *CD11b* Gene and Phylogenetic Analysis of the α-Integrin Gene Family Demonstrate Remarkable Conservation of Genomic Organization and Suggest Early Diversification during Evolution", pages 480-490, see entire document.	1-38

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

In..national application No.
PCT/US94/14832

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

C07H 19/00, 21/00; C12N 5/00, 15/00, 1/20; C12P 21/06; C12Q 1/68, 1/00; C07K 1/00, 2/00, 4/00, 14/00, 16/00; A61K 35/14

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

435/6, 7.1, 69.1, 240.2, 252.3, 320.1; 530/350, 387.1, 387.2, 388.1, 388.22; 536/22.1, 23.1, 23.5